Listing of Claims

1. **(Currently Amended)** A method for generating at least one error-corrected experiment profile of at least one experiment profile in a plurality of pairs of profiles $\{A_m,C_m\}$, where m = 1, 2, …, M, and M is the number of the pairs of profiles; and wherein, for each $m \in \{1, 2, \ldots, M\}$, A_m is an experiment profile, and C_m is a reference profile; and wherein $\{A_m\}$ represents experiment profiles in said plurality of pairs of profiles $\{A_m,C_m\}$ and $\{C_m\}$ represents reference profiles in said plurality of pairs of profiles $\{A_m, C_m\}$, said method comprising:

(a) calculating, on a **suitably programmed** computer, an average reference profile $\bar{C}$ of said plurality of reference profiles $\{C_m\}$ where m = 1, 2, …, M;

(b) determining, on a **suitably programmed** computer, for at least one profile pair $\{A_m,C_m\}$where $m \in \{1, 2, \ldots, M\}$ of said plurality of pairs of profiles $\{A_m, C_{m,}\}$ a differential reference profile computed between C_m and $\bar{C}$;

(c) adjusting, on a **suitably programmed** computer, an experiment profile A_m of said at least one profile pair $\{A_m, C_m\}$ where $m \in \{1, 2, \ldots, M\}$ based on said differential reference profile determined for said profile pair to generate a first error-corrected experiment profile A'_m for each $m \in \{1, 2, \ldots, M\}$, wherein said experiment profile A_m comprises a first data set, said reference profile C_m comprises a second data set, said average reference profile $\bar{C}$ comprises data set $\{\bar{C}\ (k)\}$, and said first error-corrected experiment profile A'_m comprises data set $\{A'_m\ (k)\}$; wherein said first data set comprises measurements or transformed measurements of a plurality of different cellular

constituents measured in a sample having been subject to a first condition, said second data set comprises measurements or transformed measurements of said plurality of different cellular constituents measured in a sample having been subject to a second condition; and wherein k = 1, 2, ..., N; k is an index of measurements or transformed measurements of said plurality of different cellular constituents, N being the total number of measurements or transformed measurements; and

(d) outputting to a user, a user interface device, a computer readable storage medium, or a local or remote computer system; or displaying: said first error-corrected experiment profile A'_m, said data set $\{A'_m(k)\}$, a second error-corrected experiment profile A''_m, or a data set $\{A''_m(k)\}$, wherein said second error-corrected experiment profile A''_m comprises said data set $\{A''_m(k)\}$ obtained by combining said first error-corrected experiment profile A'_m with said experiment profile A_m using a weighing factor $\{w(k)\}$, k = 1, 2, ... , N, wherein $w(k)$ is a weighing factor for the k'th measurement.

2. (Previously Presented) The method of claim 1, wherein said steps (b) and (c) are performed for each profile pair $\{A_m, C_m\}$ where $m \in \{1, 2, \ldots, M\}$.

3. (Previously Presented) The method of claim 2, wherein each of said experiment profile A_m and said reference profile C_m comprises measurements or transformed measurements of said plurality of different cellular constituents from the same experimental reaction.

4. (Previously Presented) The method of claim 3, wherein said $\bar{C}(k)$ is calculated according to the equation

$$\bar{C}(k) = \frac{1}{M}\sum_{m=1}^{M} C_m(k)$$

wherein said differential reference profile is determined according to the equation

$$C_{diff}(m,k) = C_m(k) - \bar{C}(k)$$

and wherein said first error-corrected experiment profile A'_m is generated according to the equation

$$A'_m(k) = A_m(k) - C_{diff}(m,k)$$

wherein $\{A_m(k)\}$ is said first data set of experiment profile A_m.

5. (**Currently Amended**) The method of claim 4, further comprising<ins>:</ins>

(d) calculating, for each said profile pair $\{A_m, C_m\}$ said second error-corrected experiment profile A''_m; and

(e) outputting to, a user interface device, a computer readable storage medium, or a local or remote computer system; or displaying; said second error-corrected **<ins>experiment</ins>** profile A''_m or said data set $\{A''_m(k)\}$.

6. (Previously Presented) The method of claim 5, wherein said second error-corrected experiment profile A''_m is calculated according to the equation

$$A''_m(k) = (1-w(k)) \cdot A_m(k) + w(k) \cdot A'_m(k).$$

7. (Previously Presented) The method of claim 6, further comprising determining said weighing factor *w(k)* according to the equation

$$w(k) = 1 - e^{-0.5\left[\frac{\bar{C}(k)}{avg\_bkgstd}\right]^2}$$

where *avg_bkgstd* is an average background standard error.

8. (Previously Presented) The method of claim 7, further comprising determining said *avg_bkgstd* according to the equation

$$avg\_bkgstd = \frac{1}{N}\sum_{k=1}^{N}\left[\frac{1}{M}\sum_{m=1}^{M} bkgstd(m,k)\right]$$

where *bkgstd (m, k)* is background standard error of $C_m(k)$.

9. (Previously Presented) The method of claim 4, further comprising determining errors $\{\sigma'_m(k)\}$ of said data set $\{A'_m(k)\}$ in said first error-corrected experiment profile A'_m.

10. (Previously Presented) The method of claim 9, further comprising determining said errors $\{\sigma'_m(k)\}$ according to the equation

$$\sigma'_m(k) = \sqrt{\sigma_m^2(k) + mixed\_\sigma_m^2(k) - 2 \cdot Cor(k) \cdot \sigma_m(k) \cdot mixed\_\sigma_m(k)}$$

where σ_m *(k)* is the standard error of $A_m(k)$, the method further comprising determining $mixed\_\sigma_m$ *(k)* according to the equation

$$mixed\_\sigma_m(k) = \frac{\sigma_m(k) + (M-1)\cdot\sigma_{ref}(k)}{M}$$

where $\sigma_{ref}(k) = \sqrt{\frac{1}{M-1}\sum_{m}^{M} (C_m(k) - \bar{C}(k))^2}$

and where Cor(k) is a correlation coefficient between said experiment profile A_m and said reference profile C_m.

11. (Previously Presented) The method of claim 10, further comprising determining said Cor(k) according to the equation

$$Cor(k) = CorMax \cdot \left[1 - e^{-0.5\cdot\left[\frac{\bar{C}(k)}{avg\_bkgstd}\right]^2}\right]$$

where CorMax is a number between 0 and 1.

12. (Previously Presented) The method of claim 7, further comprising determining errors $\{\sigma''_m(k)\}$ of said data set $\{A''_m(k)\}$ in said second error-corrected experiment profile A''_m.

13. (Previously Presented) The method of claim 12, wherein said errors

$\{\sigma''_m(k)\}$ are determined according to the equation

$$\sigma''_m(k) = \sqrt{[1 - w(k)] \cdot \sigma_m^2(k) + w(k)\sigma'^{\,2}_m(k)}$$

where $\sigma_m(k)$ is the standard error of $A_m(k)$, the method further comprising (i) determining $\sigma'_m(k)$ according to the equation

$$\sigma'_m(k) = \sqrt{\sigma_m^2(k) + mixed\_\sigma_m{}^2(k) - 2 \cdot Cor(k) \cdot \sigma_m(k) \cdot mixed\_\sigma_m(k)}, \text{ and}$$

(ii) determining $mixed\_\sigma_m(k)$ according to the equation

$$mixed\_\sigma_m(k) = \frac{\sigma_m(k) + (M-1) \cdot \sigma_{ref}(k)}{M}$$

where $\sigma_{ref}(k) = \sqrt{\frac{1}{M-1}\sum_m^M (c_m(k) - \bar{C}(k))^2}$

and where Cor(k) is a correlation coefficient between said experiment profile A_m and said reference profile C_m.

14. (Previously Presented) The method of claim 13, further comprising determining said Cor(k) according to the equation

$$Cor(k) = CorMax \cdot \left[1 - e^{-0.5 \cdot \left[\frac{\bar{C}(k)}{avg\_bkgstd}\right]^2}\right]$$

where CorMax is a number between 0 and 1.

15. (Previously Presented) The method of claim 2, wherein said experiment profile A_m and said reference profile C_m of each said profile pair $\{A_m, C_m\}$ are measured in a two-channel microarray experiment.

16. (Previously Presented) The method of claim 15, wherein said reference profiles $\{C_m\}$, where m = 1, 2, ... , M, are measured with samples labeled with a same label.

17. (Previously Presented) The method of claim 2, wherein at least one of said plurality of pairs of profiles $\{A_m, C_m\}$ is a virtual profile.

18. (Previously Presented) The method of claim 1, wherein said plurality of pairs of profiles $\{A_m, C_m\}$ are transformed profiles each comprising transformed measurements of said plurality of different cellular constituents in data set $\{A_m(k)\}$ and data set $\{C_m(k)\}$, respectively; and wherein said data set $\{A_m(k)\}$ is said first data set, and said data set $\{C_m(k)\}$ is said second data set.

19. (Canceled).

20. (Previously Presented) The method of claim 1, further comprising:

(a0) removing nonlinearity, prior to said calculating step (a), from measurements or transformed measurements of said plurality of different cellular constituents to generate said plurality of pairs of profiles $\{A_m, C_m\}$ comprising said

experiment profile A_m and reference profile C_m.

21. **(Currently Amended)** The method of claim 20, wherein said removing step (a0) comprises:

(a0i) calculating an average profile of pre-experiment profiles $\{A_m^{pre}\}$ and pre- reference profiles $\{C_m^{pre}\}$; wherein each of said pre-experiment profiles comprises measurements or transformed measurements of said plurality of different cellular constituents measured in said sample having been subject to said first condition ~~of said experiment~~, which when nonlinearity is removed therefrom, produces each said experiment profile A_m; and wherein each of said pre-reference profiles comprises measurements or transformed measurements of said plurality of different cellular constituents measured in said sample having been subject to said second condition ~~of said experiment~~, which when nonlinearity is removed therefrom, produces each said reference profile C_m; and

(a0ii) adjusting each of said pre-experiment profiles $\{A_m^{pre}\}$ based on first differences between each of said pre-experiment profiles $\{A_m^{pre}\}$ and said average profile, thereby generating each said experiment profile A_m; and adjusting each of pre-reference profiles $\{C_m^{pre}\}$ based on second differences between each of said pre-reference profiles $\{C_m^{pre}\}$ and said average profile, thereby generating each said reference profile C_m.

22. (Previously Presented) The method of claim 21, further comprising calculating said first differences based on a first subset of said measurements or transformed measurements of said plurality of different cellular constituents in said pre-experiment profiles $\{A_m^{pre}\}$ and said average profile; and calculating said second differences based on a second subset of said measurements or transformed measurements of said plurality of different cellular constituents in said pre-reference profiles $\{C_m^{pre}\}$ and said average profile.

23. (Previously Presented) The method of claim 22, wherein said first subset consists of measurements or transformed measurements of said plurality of different cellular constituents that are ranked similarly between each of said pre-experiment profiles $\{A_m^{pre}\}$ and said average profile, and said second subset consists of measurements or transformed measurements of said plurality of different cellular constituents that are ranked similarly between each of said pre-reference profiles $\{C_m^{pre}\}$ and said average profile.

24. (Previously Presented) The method of claim 23, wherein said adjusting step (a0ii) is carried out by a method comprising:

(ii1) binning said first subset into a first plurality of bins, wherein each of said first plurality of bins consists of measurements or transformed measurements of said plurality of different cellular constituents in one of said pre-experiment

profiles $\{A_{m}^{pre}\}$ and said average profile having a value in a given range; and binning said second subset into a second plurality of bins, wherein each of said second plurality of bins consists of measurements or transformed measurements of said plurality of different cellular constituents in one of said pre-reference profiles $\{C_{m}^{pre}\}$and said average profile having a value in a given range;

(ii2) calculating, in each bin of said first plurality of bins, a first mean difference between a feature value of measurements or transformed measurements of said one of said pre-experiment profiles $\{A_{m}^{pre}\}$ and a feature value of said average profile, and calculating a second mean difference between a feature value of measurements or transformed measurements of said one of said pre-reference profiles $\{C_{m}^{pre}\}$ and a feature value of said average profile;

(ii3) determining a first curve of said first mean difference as a first function of values of measurements or transformed measurements of said plurality of different cellular constituents for said one of said pre-experiment profiles $\{A_{m}^{pre}\}$,wherein said first function is represented by, $nonlinear\_A_{m}^{pre}$; and determining a second curve of said second mean difference as a second function of values of measurements or transformed measurements of said plurality of different cellular constituents for said one of said pre-reference profiles $\{C_{m}^{pre}\}$,wherein said second function is represented by $nonlinear\_C_{m}^{pre}$; and

(ii4) adjusting each of said pre-experiment profiles $\{A_m^{pre}\}$ according to the equation:

$$A_m(k) = A_m^{pre}(k) - nonlinear\_A_m^{pre}(k),$$

and adjusting each of said pre-reference profiles $\{C_m^{pre}\}$ according to the equation:

$$C_m(k) = C_m^{pre}(k) - nonlinear\_C_m^{pre}(k),$$

where k = 1, ..., N; and where $A_m^{pre}(k)$ and $C_m^{pre}(k)$ are data sets of each of said pre-experiment profiles $\{A_m^{pre}\}$ and each of said pre-reference profiles $\{C_m^{pre}\}$, respectively; and where $A_m(k)$ and $C_m(k)$ are said first data set and said second data set, respectively.

25. (Previously Presented) The method of claim 1, further comprising:

(a0) normalizing, prior to said calculating step (a), measurements or transformed measurements of said plurality of different cellular constituents in a pre-experiment profile A_m^{pre} and a pre-reference profile C_m^{pre} to generate said experiment profile A_m and said reference profile C_m, respectively.

26. (Previously Presented) The method of claim 25, wherein said normalizing step (a0) comprises normalizing a data set $A_m^{pre}(k)$ and a data set $C_m^{pre}(k)$, according to the equations:

$$A_m(k) = \frac{A^{pre}_m(k) \cdot \overline{A^{pre}_m C^{pre}_m}}{\overline{A^{pre}_m}}$$

and

$$C_m(k) = \frac{C^{pre}_m(k) \cdot \overline{A^{pre}_m C^{pre}_m}}{\overline{C^{pre}_m}},$$

wherein said data sets $A^{pre}_m(k)$ and $C^{pre}_m(k)$ each comprises measurements or transformed measurements of said plurality of different cellular constituents, where $\overline{A^{pre}_m}$ is an average of measurements or transformed measurements of said plurality of different cellular constituents in said $A^{pre}_m(k)$, and $\overline{C^{pre}_m}$ is an average of measurements or transformed measurements of said plurality of different cellular constituents in said $C^{pre}_m(k)$, wherein $A_m(k)$ is said first data set, wherein $A_m(k)$ comprises normalized measurements or normalized transformed measurements of said pre-experiment profile A^{pre}_m; and $C_m(k)$ is said second data set wherein $A_m(k)$ comprises normalized measurements or normalized transformed measurements of said reference profile C^{pre}_m; and wherein $\overline{A^{pre}_m C^{pre}_m}$ is an average calculated according to the equation

$$\overline{A^{pre}_m C^{pre}_m} = \frac{1}{2M} \sum_{m=1}^{M} (\overline{A^{pre}_m} + \overline{C^{pre}_m}).$$

27. (Previously Presented) The method of claim 26, further comprising

normalizing errors of said data sets { $A_m^{pre}(k)$ } and { $C_m^{pre}(k)$ }, respectively, according to the equations:

$$\sigma_m^{NA}(k) = \frac{\sigma_m^{preA}(k) \cdot \overline{A_m^{pre} C_m^{pre}}}{\overline{A_m^{pre}}}$$

and

$$\sigma_m^{NC}(k) = \frac{\sigma_m^{preC}(k) \cdot \overline{A_m^{pre} C_m^{pre}}}{\overline{C_m^{pre}}},$$

where $\sigma_m^{preA}(k)$ and $\sigma_m^{preC}(k)$ are the standard errors of $A_m^{pre}(k)$ and $C_m^{pre}(k)$, respectively, and $\sigma_m^{NA}(k)$ and $\sigma_m^{NC}(k)$ are normalized standard errors of $A_m(k)$ and $C_m(k)$, respectively.

28. (Previously Presented) The method of claim 27, further comprising normalizing background errors of said data sets { $A_m^{pre}(k)$ } and { $C_m^{pre}(k)$ }, respectively, according to the equations:

$$bkgstd_m^{NA}(k) = \frac{bkgstd_m^{preA}(k) \cdot \overline{A_m^{pre} C_m^{pre}}}{\overline{A_m^{pre}}}$$

and

$$bkgstd_m^{NC}(k) = \frac{bkgstd_m^{preC}(k) \cdot \overline{A_m^{pre} C_m^{pre}}}{\overline{C_m^{pre}}}$$

where $bkgstd_m^{preA}(k)$ and $bkgstd_m^{preC}(k)$ are the standard background errors of

$A^{pre}_{m}(k)$ and $C^{pre}_{m}(k)$, respectively, and $bkgstd^{NA}_{m}(k)$ and $bkgstd^{NC}_{m}(k)$ are normalized standard background errors of $A_m(k)$ and $C_m(k)$, respectively.

29. (Previously Presented) The method of claim 28, further comprising calculating said averages $\overline{A^{pre}_{m}}$ and $\overline{C^{pre}_{m}}$ by excluding measurements or transformed measurements of said plurality of different cellular constituents having a value among the highest 10% of said measurements or transformed measurements of said plurality of different cellular constituents in said data sets $\{A^{pre}_{m}(k)\}$ and $\{C^{pre}_{m}(k)\}$, respectively.

30. **(Currently Amended)** A method for generating at least one error-corrected experiment profile of at least one experiment profile in a plurality of pairs of profiles $\{XA_m, XC_m\}$, XA_m being an experiment profile, XC_m being a reference profile, where m = 1, 2, ... , M, M is the number of pairs of profiles, said method comprising:

(a) processing, on a **suitably programmed** computer, said plurality of pairs of profiles $\{XA_m, XC_m\}$ to obtain a plurality of pairs of processed profiles $\{PA_m, PC_m\}$, PA_m being a processed experiment profile, PC_m being a processed reference profile;

(b) calculating, on a **suitably programmed** computer, an average processed

reference profile $\overline{PC}$ of processed reference profiles $\{PC_m\}$, where m = 1,2, ..., M;

(c) determining, on a **suitably programmed** computer, for at least one processed profile pair $\{PA_m, PC_m\}$ where $m \in \{1, 2, ..., M\}$ of said plurality of pairs of processed profiles $\{PA_m, PC_m\}$, where m = 1, 2, ..., M, a differential reference profile computed between PC_m and $\overline{PC}$;

(d) adjusting, on a **suitably programmed** computer, a processed experiment profile PA_m of said at least one processed profile pair $\{PA_m, PC_m\}$ where $m \in \{1, 2, ..., M\}$ using said differential reference profile determined for said at least one processed profile pair to generate a first error-corrected processed experiment profile PA'_m ; wherein for each $m \in \{1, 2, ..., M\}$, said processed experiment profile PA_m comprises a first processed data set, said processed reference profile PC_m comprises a second processed data set, said average processed reference profile $\overline{PC}$ comprises data set $\{\overline{PC}(k)\}$, said first error-corrected processed experiment profile PA'_m comprises dataset $\{PA'_m(k)\}$, said experiment profile XA_m comprises data set $\{XA_m(k)\}$, said reference profile XC_m comprises data set $\{XC_m(k)\}$, wherein said data set $\{XA_m(k)\}$ comprises measurements of a plurality of different cellular constituents measured in a sample having been subject to a first condition, said data set $\{XC_m(k)\}$ comprises measurements of said plurality of different cellular constituents measured in a sample having been subject to a second condition, and where k = 1, 2, ..., N; k is an index of measurements of cellular constituents, N being the total number of measurements; and

(e) outputting to a user, a user interface device, a computer readable storage medium, or a local or remote computer system; or displaying: said first error-corrected processed experiment profile PA'_m, said data set{ $PA'_m(k)$}, a second error-corrected processed experiment profile PA''_m, or a data set $\{PA''_m(k)\}$, wherein said second error-corrected processed experiment profile PA''_m comprises said data set $\{PA''_m(k)\}$obtained by combining said first error-corrected processed experiment profile PA'_m with said processed experiment profile PA_m using a weighing factor $\{w(k)\}$, k = 1 , 2, ..., N, wherein $w(k)$ is a weighing factor for the k'th measurement.

31. (Previously presented) The method of claim 30, wherein said processing step (a) comprises normalizing each said experiment profile XA_m and reference profile XC_m.

32. (Previously presented) The method of claim 31, wherein said normalizing is carried out according to the equations:

$$NA_m(k) = \frac{XA_m(k)\cdot\overline{XAC}}{\overline{XA_m}}$$

and

$$NC_m(k) = \frac{XC_m(k)\cdot\overline{XAC}}{\overline{XC_m}}$$

where $\{NA_m(k)\}$ is said first data set of said processed experiment profile PA_m, and $\{NC_m(k)\}$ is said second data set of said processed reference profile PC_m; where

$\overline{XA_m}$ is an average of measurements or transformed measurements of said plurality of different cellular constituents of said data set $\{XA_m(k)\}$, and $\overline{XC_m}$ is an average of measurements or transformed measurements of said plurality of different cellular constituents of data set $\{XC_m(k)\}$; and wherein $\overline{XAC}$ is an average calculated according to the equation

$$\overline{XAC} = \frac{1}{2M} \sum_{m=1}^{M} (\overline{XA_m} + \overline{XC_m}).$$

33. **(Currently Amended)** The method of claim 32, further comprising normalizing errors of said experiment profile XA_m and reference profile XC_m according to the equations:

$$\sigma_m^A(k) = \frac{\sigma_m^{XA}(k) \cdot \overline{XAC}}{\overline{XA_m}}$$

and

$$\sigma_m^C(k) = \frac{\sigma_m^{XC}(k) \cdot \overline{XAC}}{\overline{XC_m}}$$

where $\sigma_m^{XA}(k)$ and $\sigma_m^{XC}(k)$ are the standard errors of $XA_m(k)$ and $XC_m(k)$, respectively, and $\sigma_m^A(k)$and $\sigma_m^C(k)$ are normalized standard errors of $NA_m(k)$ and ~~$NA_m(k)$~~ $\underline{NC_m(k)}$, respectively.

34. **(Currently Amended)** The method of claim 33, further comprising normalizing background errors of said experiment profile XA_m and reference profile XC_m according to the equations:

$$bkgstd_m^A(k) = \frac{bkgstd_m^{XA}(k) \cdot \overline{XAC}}{\overline{XA_m}}$$

and

$$bkgstd_m^C(k) = \frac{bkgstd_m^{XC}(k) \cdot \overline{XAC}}{\overline{XC_m}}$$

where $bkgstd_m^{XA}(k)$ and $bkgstd_m^{XC}(k)$ are the standard background errors of $XA_m(k)$ and $XC_m(k)$, respectively, and $bkgstd_m^A(k)$ and $bkgstd_m^C(k)$ are normalized standard background errors of said $NA_m(k)$ and said ~~$NA_m(k)$~~ **$\underline{NC_m(k)}$**, respectively.

35. (Previously presented) The method of claim 33, further comprising determining said averages $\overline{XA_m}$ and $\overline{XC_m}$ excluding measurements of said plurality of different cellular constituents having a value among the highest 10% of said measurements or transformed measurements of said plurality of different cellular constituents in said data sets $\{XA_m(k)\}$ and $\{XC_m(k)\}$, respectively.

36. **(Currently Amended)** The method of claim 30, wherein said processing step (a) comprises:

normalizing each said experiment profile XA_m and reference profile XC_m to

generate normalized data set $\{NA_m(k)\}$ and normalized data set $\{NC_m(k)\}$, respectively;

~~and~~

transforming said normalized data set $\{NA_m(k)\}$ to obtain a transformed data set $\{TA_m(k)\}$, where said transformed data set $\{TA_m(k)\}$ is said first data set of said processed experiment profile PA_m; and

transforming said normalized data set $\{NC_m(k)\}$ to obtain a transformed data set $\{TC_m(k)\}$, where said transformed data set $\{TC_m(k)\}$ is said second data set of said processed reference profile PC_m.

37. **(Currently Amended)** The method of claim 36, wherein said transforming is carried out **<u>for an experiment</u>** according to the equations

$$TA_m(k) = f(x) = \frac{1n\left[\frac{b^2+2\cdot a^2\cdot NA_m(k)}{a} + 2\cdot\sqrt{c^2+b^2\cdot NA_m(k)+a^2\cdot[NA_m(k)]^2}\right]}{a} + d,$$

for $NA_m(k)>0$

and

$$TC_m(k) = f(x) = \frac{1n\left[\frac{b^2+2\cdot a^2\cdot NC_m(k)}{a} + 2\cdot\sqrt{c^2+b^2\cdot NC_m(k)+a^2\cdot[NC_m(k)]^2}\right]}{a} + d,$$

for $NC_m(k)>0$

where d is described by the equation

$$d = \frac{-1n\left[\frac{b^2}{a}+2\cdot c\right]}{a}$$

and where a is the fractional error coefficient of said experiment, b is the Poisson error coefficient of said experiment, and c is the standard deviation of background

noise of said experiment.

38. **(Currently Amended)** The method of claim 30, wherein said processing step (a) comprises:

normalizing each said experiment profile XA_m and reference profile XC_m to generate normalized data set $\{NA_m(k)\}$ and normalized data set $\{NC_m(k)\}$, respectively;

transforming said normalized data set $\{NA_m(k)\}$ to obtain a transformed data set $\{TA_m(k)\}$; ~~and~~

transforming said normalized data set $\{NC_m(k)\}$ to obtain a transformed data set $\{TC_m(k)\}$; and

removing nonlinearity from each said transformed data sets $\{TA_m(k)\}$ and $\{TC_m(k)\}$, respectively.

39. (Previously Presented) The method of claim 38, wherein said removing nonlinearity is carried out by a method comprising

(a1) calculating an average transformed profile of transformed experiment profiles and transformed reference profiles, wherein each of said transformed experiment profiles contains a corresponding transformed data set $\{TA_m(k)\}$, and each of said transformed reference profiles contains a corresponding transformed data set $\{TC_m(k)\}$; and

(a2) adjusting each of said transformed experiment profiles based on first

differences between each of said transformed experiment profiles and said average transformed profile, and adjusting each of said transformed reference profiles based on second differences between each of said transformed reference profiles and said average transformed profile.

40. (Previously Presented) The method of claim 39, further comprising calculating said first differences based on the differences in a first subset of transformed measurements of said plurality of different cellular constituents between each of said transformed experiment profiles and said average transformed profile, and calculating said second differences based on the differences in a second subset of transformed measurements of said plurality of different cellular constituents between each of said transformed reference profiles and said average transformed profile.

41. (Previously Presented) The method of claim 40, wherein each said first subset consists of transformed measurements that are ranked similarly between each of said transformed experiment profiles and said average transformed profile, and each said second subset consists of transformed measurements that are ranked similarly between each of said transformed reference profiles and said average transformed profile.

42. (**Currently Amended**) The method of claim 41, wherein said adjusting step (a2) is carried out by a method comprising:

(a2i) binning said first subset into a plurality of bins, each said bin consisting of

transformed measurements of said plurality of different cellular constituents in one of said transformed experiment profiles and said average transformed profile having a value in a given range; and binning said second subset into a plurality of bins, each said bin consisting of transformed measurements of said plurality of different cellular constituents in one of said transformed reference profiles and said average transformed profile having a value in a given range;

(a2ii) calculating, in each bin of said plurality of bins, a first mean difference between a feature value of transformed measurements of said plurality of different cellular constituents in said one of said transformed experiment profiles and a feature value of said average transformed profile, and calculating a second mean difference between a feature value of transformed measurements of said plurality of different cellular constituents in said one of said reference profiles and a feature value of the average profile;

(a2iii) determining a first curve of said first mean difference as a first function of values of transformed measurements of said plurality of different cellular constituents for said one of said transformed experiment profiles, wherein said first function is represented by, $nonlinear\_TA_m$, and determining a second curve of said second mean difference as a second function of values of transformed measurements of said plurality of different cellular constituents for said one of said transformed reference profiles, wherein said second function is represented by $nonlinear\_TC_m$; and

(a2iv) computing corrected transformed measurements of said plurality of

different cellular constituents in each said transformed data set $\{TA_m(k)\}$, according to the equation:

$$TA_m^{corr}(k) = TA_m(k) - nonlinear\_TA_m(k),$$

and computing corrected transformed measurements of said plurality of different cellular constituents in each said transformed data set $\{TC_m(k)\}$, according to the equation:

$$TC_m^{corr}(k) = TC_m(k) - nonlinear\_TC_m(k),$$

where k = 1, ..., N; and where $\{TA_m^{corr}(k)\}$ is said first processed data set of said processed experiment profile PA_m, and $\{TC_m^{corr}(k)\}$ is said second processed data set of said processed reference profile PC_m.

43. (Previously Presented) The method of claim 42, wherein said processed experiment profile PA_m and said processed reference profile PC_m comprise transformed measurements of said plurality of different cellular constituents from the same experimental reaction.

44. (Previously Presented) The method of claim 43, further comprising calculating $\overline{PC}(k)$ according to the equation

$$\overline{PC}(k) = \frac{1}{M} \sum_{m=1}^{M} PC_m(k),$$

wherein $\{PC_m(k)\}$ comprises transformed measurements from said second processed data

set $\{TC_{m}^{corr}(k)\}$ and calculating said differential reference profile according to the equation

$$PC_{diff}(m,k) = PC_m(k) - \overline{PC}(k)$$

and wherein said first error-corrected profile is calculated according to the equation

$$PA'_m(k) = PA_m(k) - PC_{diff}(m,k),$$

wherein $\{ PA_m(k) \}$comprises transformed measurements from said first data set $\{TA_{m}^{corr}(k)\}$.

45. (Previously Presented) The method of claim 44, further comprising

(d) calculating for each processed profile pair $\{PA_m, PC_m\}$, where $m \in \{1, 2, ..., M\}$, a second error-corrected experiment profile PA''_m comprising data set $\{PA''_m(k)\}$ by combining said first error-corrected experiment profile PA'_m with said processed experiment profile PA_m using a weighing factor $\{w(k)\}$, $k = 1,2, ..., N$, wherein $w(k)$ is a weighing factor for the k'th measurement.

46. (Previously Presented) The method of claim 45, wherein said second error-corrected experiment profile PA''_m is calculated according to the equation

$$PA''_m(k) = (1-w(k)) \cdot PA_m(k) + w(k)PA'_m(k).$$

47. (Previously Presented) The method of claim 46, further comprising determining said weighing factor according to the equation

$$w(k) = 1\text{-}e^{-0.5\left[\frac{\overline{PC}(k)}{avg\_bkgstd}\right]^2}$$

where *avg_bkgstd* is an average background standard error.

48. (Previously Presented) The method of claim 47, further comprising determining said *avg_ bkgstd* according to the equation

$$avg\_bkgstd = \frac{1}{N} \sum_{k=1}^{N} \left[\frac{1}{M} \sum_{m=1}^{M} bkgstd(m,k)\right]$$

where *bkgstd (m, k)* is background standard error of $PC_m(k)$.

49. (Previously Presented) The method of claim 44, further comprising determining errors $\{P\sigma'_m\}$ of said first error-corrected experiment profile $\{PA'_m\}$, wherein said $\{P\sigma'_m\}$ comprises error data set $\{P\sigma'_m(k)\}$.

50. (Previously Presented) The method of claim 49, further comprising determining said error data set $\{P\sigma'_m(k)\}$ according to the equation

$$\sigma'_m(k) = \sqrt{P\sigma_m^2(k) = mixed\_P\sigma_m{}^2(k) - 2Cor(k) \cdot P\sigma_m(k) \cdot mixed\_P\sigma_m(k)}$$

where $P\sigma_m(k)$ is the standard error of $A_m(k)$, and determining $mixed\_P\sigma_m(k)$ according to the equation

$$mixed\_P\sigma_m(k) = \frac{P\sigma_m(k) + (M-1)\cdot P\sigma_{ref}(k)}{M}$$

where

$$P\sigma_{ref}(k) = \sqrt{\frac{1}{M-1}\sum_{m}^{M} (PC_m(k) - \overline{PC}(k))^2}$$

and where Cor(k) is a correlation coefficient between said processed experiment profile PA_m and said processed reference profile PC_m.

51. (Previously Presented) The method of claim 50, wherein said Cor(k) is determined according to the equation

$$Cor(k) = CorMax \cdot \left[1 - e^{-0.5\left[\frac{\overline{PC}(k)}{avg\_bkgstd}\right]^2}\right]$$

where CorMax is a number between 0 and 1.

52. (Previously Presented) The method of claim 51, further comprising determining errors $\{P\sigma''_m\}$ of said second error-corrected experiment profile $\{PA''_m\}$ wherein said $\{P\sigma''_m\}$ comprises error data set $\{P\sigma''_m(k)\}$.

53. (Previously Presented) The method of claim 52, further comprising determining said error data set $\{P\sigma''_m(k)\}$ according to the equation

$$P\sigma''_m(k) = \sqrt{[1 - w(k)] \cdot P\sigma_m^2(k) + w(k)P\sigma'^2_m(k)}$$

where $P\sigma_m(k)$ is the standard error of $PA_m(k)$, and further comprising determining $P\sigma'_m(k)$ according to the equation

$$P\sigma'_m(k) =$$

$\sqrt{P\sigma_m^{\,2}(k) + mixed\_P\sigma_m{}^2(k) - 2 \cdot Cor(k) \cdot P\sigma_m(k) \cdot mixed\_P\sigma_m(k)}$, and

further comprising determining $mixed\_P\sigma_m(k)$ according to the equation

$$mixed\_P\sigma_m(k) = \frac{P\sigma_m(k) + (M-1) \cdot P\sigma_{ref}(k)}{M}$$

where

$$P\sigma_{ref}(k) = \sqrt{\frac{1}{M-1} \sum_{m}^{M} (PC_m(k) - \overline{PC}(k))^2}$$

and where Cor(k) is a correlation coefficient between said processed experiment profile PA_m and said processed reference profile PC_m.

54. (Previously Presented) The method of claim 53, further comprising determining said Cor(k) according to the equation

$$Cor(k) = CorMax \cdot \left[1 - e^{-0.5\left[\frac{\overline{PC}(k)}{avg\_bkgstd}\right]^2}\right]$$

where CorMax is a number between 0 and 1.

55. (Previously Presented) The method of claim 54, wherein each said pair of profiles XA_m and XC_m comprise measurements of said plurality of different cellular constituents from a two-channel microarray experiment.

56. (Previously Presented) The method of claim 55, wherein said reference profiles $\{XC_m\}$, m = 1, 2, ... , M, are measured with samples labeled with a same

label.

57. (Previously Presented) The method of claim 56, wherein at least one of said pairs of profiles $\{XA_m, XC_m\}$ is a virtual profile.

58. **(Canceled)**

59. **(Canceled)**

60. (Canceled).

61. (Canceled).

62. (Canceled).

63. (Canceled).

64. (Canceled).

65. (Canceled).

66. (**Currently Amended**) A method for generating at least one error-corrected experiment profile of at least one experiment profile A_m, where $m \in \{1, 2, ..., M\}$ in at least one of a plurality of pairs of profiles $\{A_m, C_m\}$, A_m being an experiment profile, C_m being a reference profile, where $m = 1, 2, \dots, M$, M is the number of pairs of profiles, said method comprising:

adjusting, on a **suitably programmed** computer, said experiment profile A_m using a differential reference profile calculated between C_m and an average reference profile $\bar{C}$ determined for ~~said~~ profile pair $\{A_m, C_m\}$ where $m \in \{1, 2, \ldots, M\}$ to generate ~~an~~ **a first** error-corrected experiment profile A'_m; wherein said average reference profile $\bar{C}$ is an average of reference profiles $\{C_m\}$, $m = 1, 2, \ldots, M$; wherein for each $m \in \{1, 2, \ldots, M\}$, said **first** error-corrected experiment profile A'_m comprises data set $\{A'_m(k)\}$, said experiment profile A_m comprises data set $\{A_m(k)\}$, said reference profile C_m comprises data set $\{C_m(k)\}$, and said average reference profile $\bar{C}$ comprises data set $\{\bar{C}(k)\}$, wherein said data set $\{A_m(k)\}$ comprises measurements or transformed measurements of a plurality of different cellular constituents measured in a sample having been subject to a first condition, said data set $\{C_m(k)\}$ comprises measurements or transformed measurements of said plurality of different cellular constituents measured in a sample having been subject to a second condition, wherein $k = 1, 2, \ldots, N$; k is an index of measurements or transformed measurements of cellular constituents, N being the total number of measurements; and

outputting to a user, a user interface device, a computer readable storage medium, or a local or remote computer system; or displaying: said first error-corrected **experiment** profile A'_m, said data set $\{A'_m(k)\}$, a second error-corrected **experiment** profile A''_m, or a data set $\{A''_m(k)\}$, wherein said second error-corrected **experiment** profile A''_m comprises said data set $\{A''_m(k)\}$ obtained by combining said first error-corrected experiment profile A'_m with said experiment profile A_m

using a weighing factor $\{w(k)\}$, k = 1, 2, ... , N, wherein *w(k)* is a weighing factor for the *k*'th measurement.

67. **(Currently Amended)** The method of claim 18, further comprising obtaining said transformed measurements of said data set $\{A_m(k)\}$ and said data set $\{C_m(k)\}$ **<u>for an experiment</u>** according to the equations:

$$A_m(k) = f(x) = \frac{1n\left[\frac{b^2+2\cdot a^2\cdot XA_m(k)}{a}+2\cdot\sqrt{c^2+b^2\cdot XA_m(k)+a^2\cdot[XA_m(k)]^2}\right]}{a} + d,$$

for XA_m(k)>0

and

$$C_m(k) = f(x) = \frac{1n\left[\frac{b^2+2\cdot a^2\cdot XC_m(k)}{a}+2\cdot\sqrt{c^2+b^2\cdot XC_m(k)+a^2\cdot[XC_m(k)]^2}\right]}{a} + d,$$

for XC_m(k)>0

where $\{XA_m(k)\}$ and $\{XC_m(k)\}$ are data sets comprising measurements of said plurality of different cellular constituents that when transformed produce said transformed measurements of said plurality of different cellular constituents of said data set $A_m(k)$ and said data set $C_m(k)$, respectively, where *d* is described by the equation:

$$d = \frac{-1n\left[\frac{b^2}{a}+2\cdot c\right]}{a}$$

and where *a* is the fractional error coefficient of said experiment, *b* is the Poisson error coefficient of said experiment, and *c* is the standard deviation of background

noise of said experiment.

68. **(Canceled)**

69. **(Canceled)**

70. (Previously Presented) The method of claim 30, wherein said processing comprises:

normalizing, transforming, and/or removing nonlinearity from measurements of said plurality of cellular constituents of said data set $\{XA_m(k)\}$ of said experiment profile XA_m, and from measurements of said plurality of cellular constituents of said data set $\{XC_m(k)\}$ of said reference profile XC_m.

71. **(New)** A computer program product for use in conjunction with a computer having a processor and a memory connected to the processor, said computer program product comprising a computer readable storage medium having a computer program mechanism encoded thereon, wherein said computer program mechanism may be loaded into the memory of said computer and cause said computer to carry out a method for generating at least one error-corrected experiment profile of at least one experiment profile in a plurality of pairs of profiles $\{A_m, C_m\}$, where $m = 1, 2, \ldots, M$, and M is the number of the pairs of profiles; and wherein, for each $m \in \{1, 2, \ldots, M\}$, A_m is an experiment profile, and C_m is a reference profile; and wherein

$\{A_m\}$ represents experiment profiles in said plurality of pairs of profiles $\{A_m, C_m\}$ and $\{C_m\}$ represents reference profiles in said plurality of pairs of profiles $\{A_m, C_m\}$, said method comprising:

(a) calculating, on a computer, an average reference profile $\bar{C}$ of said plurality of reference profiles $\{C_m\}$ where m = 1, 2, …, M;

(b) determining, on a computer, for at least one profile pair $\{A_m, C_m\}$ where $m \in \{1, 2, \ldots, M\}$ of said plurality of pairs of profiles $\{A_m, C_{m,}\}$ a differential reference profile computed between C_m and $\bar{C}$;

(c) adjusting, on a computer, an experiment profile A_m of said at least one profile pair $\{A_m, C_m\}$ where $m \in \{1, 2, \ldots, M\}$ based on said differential reference profile determined for said profile pair to generate a first error-corrected experiment profile A'_m for each $m \in \{1, 2, \ldots, M\}$, wherein said experiment profile A_m comprises a first data set, said reference profile C_m comprises a second data set, said average reference profile $\bar{C}$ comprises data set $\{\bar{C}(k)\}$, and said first error-corrected experiment profile A'_m comprises data set $\{A'_m(k)\}$; wherein said first data set comprises measurements or transformed measurements of a plurality of different cellular constituents measured in a sample having been subject to a first condition, said second data set comprises measurements or transformed measurements of said plurality of different cellular constituents measured in a sample having been subject to a second condition; and wherein k = 1, 2, ..., N; k is an index of measurements or transformed measurements of said plurality of different cellular constituents, N being the total number of

measurements or transformed measurements; and

(d) outputting to a user, a user interface device, a computer readable storage medium, or a local or remote computer system; or displaying: said first error-corrected experiment profile A'_m, said data set $\{A'_m(k)\}$, a second error-corrected experiment profile A''_m, or a data set $\{A''_m(k)\}$, wherein said second error-corrected experiment profile A''_m comprises said data set $\{A''_m(k)\}$ obtained by combining said first error-corrected experiment profile A'_m with said experiment profile A_m using a weighing factor $\{w(k)\}$, $k = 1, 2, \ldots, N$, wherein $w(k)$ is a weighing factor for the k'th measurement.

72. (**New**) The computer program product of claim 71, wherein said steps (b) and (c) are performed for each profile pair $\{A_m, C_m\}$ where $m \in \{1, 2, \ldots, M\}$.

73. (**New**) The computer program product of claim 72, wherein each of said experiment profile A_m and said reference profile C_m comprises measurements or transformed measurements of said plurality of different cellular constituents from the same experimental reaction.

74. (**New**) The computer program product of claim 73, wherein said $\bar{C}(k)$ is calculated according to the equation

$$\bar{C}(k) = \frac{1}{M}\sum_{m=1}^{M} C_m(k)$$

wherein said differential reference profile is determined according to the equation

$$C_{diff}(m,k) = C_m(k) - \bar{C}(k)$$

and wherein said first error-corrected experiment profile A'_m is generated according to the equation

$$A'_m(k) = A_m(k) - C_{diff}(m,k)$$

wherein $\{A_m(k)\}$ is said first data set of experiment profile A_m.

75. **(New)** The computer program product of claim 74, wherein the method further comprises:

(d) calculating, for each said profile pair $\{A_m, C_m\}$ said second error-corrected experiment profile A''_m; and

(e) outputting to, a user interface device, a computer readable storage medium, or a local or remote computer system; or displaying; said second error-corrected experiment profile A''_m or said data set $\{A''_m(k)\}$.

76. **(New)** The computer program product of claim 75, wherein said second error-corrected experiment profile A''_m is calculated according to the equation

$$A''_m(k) = (1\text{-}w(k)) \cdot A_m(k) + w(k) \cdot A'_m(k).$$

77. (**New**) The computer program product of claim 76, wherein the method further comprises determining said weighing factor *w(k)* according to the equation

$$w(k) = 1 - e^{-0.5\left[\frac{\bar{C}(k)}{avg\_bkgstd}\right]^2}$$

where *avg_bkgstd* is an average background standard error.

78. (**New**) The computer program product of claim 77, wherein the method further comprises determining said *avg_bkgstd* according to the equation

$$avg\_bkgstd = \frac{1}{N} \sum_{k=1}^{N} \left[\frac{1}{M} \sum_{m=1}^{M} bkgstd(m,k)\right]$$

where *bkgstd (m, k)* is background standard error of $C_m(k)$.

79. (**New**) The computer program product of claim 74, wherein the method further comprises determining errors $\{\sigma'_m(k)\}$ of said data set $\{A'_m(k)\}$ in said first error-corrected experiment profile A'_m.

80. (**New**) The computer program product of claim 79, wherein the method further comprises determining said errors $\{\sigma'_m(k)\}$ according to the equation

$$\sigma'_m(k) = \sqrt{\sigma_m^2(k) + mixed\_\sigma_m^2(k) - 2 \cdot Cor(k) \cdot \sigma_m(k) \cdot mixed\_\sigma_m(k)}$$

where σ_m *(k)* is the standard error of $A_m(k)$, the method further comprising determining $mixed\_\sigma_m$ *(k)* according to the equation

$$mixed\_\sigma_m(k) = \frac{\sigma_m(k) + (M-1)\cdot\sigma_{ref}(k)}{M}$$

where $\sigma_{ref}(k) = \sqrt{\frac{1}{M-1}\sum_{m}^{M} (C_m(k) - \bar{C}(k))^2}$

and where Cor(k) is a correlation coefficient between said experiment profile A_m and said reference profile C_m.

81. **(New)** The computer program product of claim 80, wherein the method further comprises determining said Cor(k) according to the equation

$$Cor(k) = CorMax \cdot \left[1 - e^{-0.5\cdot\left[\frac{\bar{C}(k)}{avg\_bkgstd}\right]^2}\right]$$

where CorMax is a number between 0 and 1.

82. **(New)** The computer program product of claim 77, wherein the method further comprises determining errors $\{\sigma''_m(k)\}$ of said data set $\{A''_m(k)\}$ in said second error-corrected experiment profile A''_m.

83. **(New)** The computer program product of claim 82, wherein said errors $\{\sigma''_m(k)\}$ are determined according to the equation

$$\sigma''_m(k) = \sqrt{[1 - w(k)] \cdot \sigma_m^2(k) + w(k)\sigma'_m{}^2(k)}$$

where $\sigma_m(k)$ is the standard error of $A_m(k)$, the method further comprising (i) determining $\sigma'_m(k)$ according to the equation

$$\sigma'_m(k) = \sqrt{\sigma_m^2(k) + mixed\_\sigma_m{}^2(k) - 2 \cdot Cor(k) \cdot \sigma_m(k) \cdot mixed\_\sigma_m(k)},$$ and

(ii) determining $mixed\_\sigma_m(k)$ according to the equation

$$mixed\_\sigma_m(k) = \frac{\sigma_m(k) + (M-1) \cdot \sigma_{ref}(k)}{M}$$

where $\sigma_{ref}(k) = \sqrt{\frac{1}{M-1}\sum_m^M (c_m(k) - \bar{C}(k))^2}$

and where Cor(k) is a correlation coefficient between said experiment profile A_m and said reference profile C_m.

84. (**New**) The computer program product of claim 83, wherein the method further comprises determining said Cor(k) according to the equation

$$Cor(k) = CorMax \cdot \left[1 - e^{-0.5 \cdot \left[\frac{\bar{C}(k)}{avg\_bkgstd}\right]^2}\right]$$

where CorMax is a number between 0 and 1.

85. (**New**) The computer program product of claim 72, wherein said

experiment profile A_m and said reference profile C_m of each said profile pair $\{A_m, C_m\}$ are measured in a two-channel microarray experiment.

86. **(New)** The computer program product of claim 85, wherein said reference profiles $\{C_m\}$, where $m = 1, 2, \ldots, M$, are measured with samples labeled with a same label.

87. **(New)** The computer program product of claim 72, wherein at least one of said plurality of pairs of profiles $\{A_m, C_m\}$ is a virtual profile.

88. **(New)** The computer program product of claim 71, wherein said plurality of pairs of profiles $\{A_m, C_m\}$ are transformed profiles each comprising transformed measurements of said plurality of different cellular constituents in data set $\{A_m(k)\}$ and data set $\{C_m(k)\}$, respectively; and wherein said data set $\{A_m(k)\}$ is said first data set, and said data set $\{C_m(k)\}$ is said second data set.

89. **(New)** The computer program product of claim 71, wherein the method further comprises:

(a0) removing nonlinearity, prior to said calculating step (a), from measurements or transformed measurements of said plurality of different cellular constituents to generate said plurality of pairs of profiles $\{A_m, C_m\}$ comprising said experiment profile A_m and reference profile C_m.

90. (**New**) The computer program product of claim 89, wherein said removing step (a0) comprises:

(a0i) calculating an average profile of pre-experiment profiles $\{A_m^{pre}\}$ and pre- reference profiles $\{C_m^{pre}\}$; wherein each of said pre-experiment profiles comprises measurements or transformed measurements of said plurality of different cellular constituents measured in said sample having been subject to said first condition, which when nonlinearity is removed therefrom, produces each said experiment profile A_m; and wherein each of said pre-reference profiles comprises measurements or transformed measurements of said plurality of different cellular constituents measured in said sample having been subject to said second condition, which when nonlinearity is removed therefrom, produces each said reference profile C_m; and

(a0ii) adjusting each of said pre-experiment profiles $\{A_m^{pre}\}$ based on first differences between each of said pre-experiment profiles $\{A_m^{pre}\}$ and said average profile, thereby generating each said experiment profile A_m; and adjusting each of pre-reference profiles $\{C_m^{pre}\}$ based on second differences between each of said pre-reference profiles $\{C_m^{pre}\}$ and said average profile, thereby generating each said reference profile C_m.

91. (**New**) The computer program product of claim 90, wherein the method

further comprises calculating said first differences based on a first subset of said measurements or transformed measurements of said plurality of different cellular constituents in said pre-experiment profiles $\{A_m^{pre}\}$ and said average profile; and calculating said second differences based on a second subset of said measurements or transformed measurements of said plurality of different cellular constituents in said pre-reference profiles $\{C_m^{pre}\}$ and said average profile.

92. **(New)** The computer program product of claim 91, wherein said first subset consists of measurements or transformed measurements of said plurality of different cellular constituents that are ranked similarly between each of said pre-experiment profiles $\{A_m^{pre}\}$ and said average profile, and said second subset consists of measurements or transformed measurements of said plurality of different cellular constituents that are ranked similarly between each of said pre-reference profiles $\{C_m^{pre}\}$ and said average profile.

93. **(New)** The computer program product of claim 92, wherein said adjusting step (a0ii) is carried out by a method comprising:

(ii1) binning said first subset into a first plurality of bins, wherein each of said first plurality of bins consists of measurements or transformed measurements of said plurality of different cellular constituents in one of said pre-experiment

profiles $\{A_m^{pre}\}$ and said average profile having a value in a given range; and binning said second subset into a second plurality of bins, wherein each of said second plurality of bins consists of measurements or transformed measurements of said plurality of different cellular constituents in one of said pre-reference profiles $\{C_m^{pre}\}$ and said average profile having a value in a given range;

(ii2) calculating, in each bin of said first plurality of bins, a first mean difference between a feature value of measurements or transformed measurements of said one of said pre-experiment profiles $\{A_m^{pre}\}$ and a feature value of said average profile, and calculating a second mean difference between a feature value of measurements or transformed measurements of said one of said pre-reference profiles $\{C_m^{pre}\}$ and a feature value of said average profile;

(ii3) determining a first curve of said first mean difference as a first function of values of measurements or transformed measurements of said plurality of different cellular constituents for said one of said pre-experiment profiles $\{A_m^{pre}\}$,wherein said first function is represented by, $nonlinear\_A_m^{pre}$; and determining a second curve of said second mean difference as a second function of values of measurements or transformed measurements of said plurality of different cellular constituents for said one of said pre-reference profiles $\{C_m^{pre}\}$,wherein said second function is represented by $nonlinear\_C_m^{pre}$; and

(ii4) adjusting each of said pre-experiment profiles $\{A_m^{pre}\}$ according to the equation:

$$A_m(k) = A_m^{pre}(k) - nonlinear\_A_m^{pre}(k),$$

and adjusting each of said pre-reference profiles $\{C_m^{pre}\}$ according to the equation:

$$C_m(k) = C_m^{pre}(k) - nonlinear\_C_m^{pre}(k),$$

where k = 1, ... , N; and where $A_m^{pre}(k)$ and $C_m^{pre}(k)$ are data sets of each of said pre-experiment profiles $\{A_m^{pre}\}$ and each of said pre-reference profiles $\{C_m^{pre}\}$, respectively; and where $A_m(k)$ and $C_m(k)$ are said first data set and said second data set, respectively.

94. **(New)** The computer program product of claim 71, wherein the method further comprises:

(a0) normalizing, prior to said calculating step (a), measurements or transformed measurements of said plurality of different cellular constituents in a pre-experiment profile A_m^{pre} and a pre-reference profile C_m^{pre} to generate said experiment profile A_m and said reference profile C_m, respectively.

95. **(New)** The computer program product of claim 94, wherein said normalizing step (a0) comprises normalizing a data set $A_m^{pre}(k)$ and a data set

$C^{pre}_{m}(k)$, according to the equations:

$$A_m(k) = \frac{A^{pre}_{m}(k)\cdot\overline{A^{pre}_{m}C^{pre}_{m}}}{\overline{A^{pre}_{m}}}$$

and

$$C_m(k) = \frac{C^{pre}_{m}(k)\cdot\overline{A^{pre}_{m}C^{pre}_{m}}}{\overline{C^{pre}_{m}}},$$

wherein said data sets $A^{pre}_{m}(k)$ and $C^{pre}_{m}(k)$ each comprises measurements or transformed measurements of said plurality of different cellular constituents, where $\overline{A^{pre}_{m}}$ is an average of measurements or transformed measurements of said plurality of different cellular constituents in said $A^{pre}_{m}(k)$, and $\overline{C^{pre}_{m}}$ is an average of measurements or transformed measurements of said plurality of different cellular constituents in said $C^{pre}_{m}(k)$, wherein $A_m(k)$ is said first data set, wherein $A_m(k)$ comprises normalized measurements or normalized transformed measurements of said pre-experiment profile A^{pre}_{m}; and $C_m(k)$ is said second data set wherein $A_m(k)$ comprises normalized measurements or normalized transformed measurements of said reference profile C^{pre}_{m}; and wherein $\overline{A^{pre}_{m}C^{pre}_{m}}$ is an average calculated according to the equation

$$\overline{A^{pre}_{m}C^{pre}_{m}} = \frac{1}{2M}\sum_{m=1}^{M}\overline{(A^{pre}_{m} + C^{pre}_{m})}.$$

96. **(New)** The computer program product of claim 95, wherein the method further comprises normalizing errors of said data sets { $A^{pre}_m(k)$ } and { $C^{pre}_m(k)$ }, respectively, according to the equations:

$$\sigma^{NA}_m(k) = \frac{\sigma^{preA}_m(k) \cdot \overline{A^{pre}_m C^{pre}_m}}{\overline{A^{pre}_m}}$$

and

$$\sigma^{NC}_m(k) = \frac{\sigma^{preC}_m(k) \cdot \overline{A^{pre}_m C^{pre}_m}}{\overline{C^{pre}_m}},$$

where $\sigma^{preA}_m(k)$ and $\sigma^{preC}_m(k)$ are the standard errors of $A^{pre}_m(k)$ and $C^{pre}_m(k)$, respectively, and $\sigma^{NA}_m(k)$ and $\sigma^{NC}_m(k)$ are normalized standard errors of $A_m(k)$ and $C_m(k)$, respectively.

97. **(New)** The computer program product of claim 96, wherein the method further comprises normalizing background errors of said data sets { $A^{pre}_m(k)$ } and { $C^{pre}_m(k)$ }, respectively, according to the equations:

$$bkgstd^{NA}_m(k) = \frac{bkgstd^{preA}_m(k) \cdot \overline{A^{pre}_m C^{pre}_m}}{\overline{A^{pre}_m}}$$

and

$$bkgstd^{NC}_m(k) = \frac{bkgstd^{preC}_m(k) \cdot \overline{A^{pre}_m C^{pre}_m}}{\overline{C^{pre}_m}}$$

where $bkgstd_m^{preA}(k)$ and $bkgstd_m^{preC}(k)$ are the standard background errors of $A_m^{pre}(k)$ and $C_m^{pre}(k)$, respectively, and $bkgstd_m^{NA}(k)$ and $bkgstd_m^{NC}(k)$ are normalized standard background errors of $A_m(k)$ and $C_m(k)$, respectively.

98. **(New)** The computer program product of claim 97, wherein the method further comprises calculating said averages $\overline{A_m^{pre}}$ and $\overline{C_m^{pre}}$ by excluding measurements or transformed measurements of said plurality of different cellular constituents having a value among the highest 10% of said measurements or transformed measurements of said plurality of different cellular constituents in said data sets $\{A_m^{pre}(k)\}$ and $\{C_m^{pre}(k)\}$, respectively.

99. **(New)** A computer program product for use in conjunction with a computer having a processor and a memory connected to the processor, said computer program product comprising a computer readable storage medium having a computer program mechanism encoded thereon, wherein said computer program mechanism may be loaded into the memory of said computer and cause said computer to carry out a method for generating at least one error-corrected experiment profile of at least one experiment profile in a plurality of pairs of profiles $\{XA_m, XC_m\}$, XA_m being an experiment profile, XC_m being a reference profile, where m = 1, 2, ... , M, M is the number of pairs of profiles, said method

comprising:

(a) processing, on a computer, said plurality of pairs of profiles $\{XA_m, XC_m\}$ to obtain a plurality of pairs of processed profiles $\{PA_m, PC_m\}$, PA_m being a processed experiment profile, PC_m being a processed reference profile;

(b) calculating, on a computer, an average processed reference profile $\overline{PC}$ of processed reference profiles $\{PC_m\}$, where m = 1,2, ..., M;

(c) determining, on a computer, for at least one processed profile pair $\{PA_m, PC_m\}$ where $m \in \{1, 2, ..., M\}$ of said plurality of pairs of processed profiles $\{PA_m, PC_m\}$, where m = 1, 2, ..., M, a differential reference profile computed between PC_m and $\overline{PC}$;

(d) adjusting, on a computer, a processed experiment profile PA_m of said at least one processed profile pair $\{PA_m, PC_m\}$ where $m \in \{1, 2, ..., M\}$ using said differential reference profile determined for said at least one processed profile pair to generate a first error-corrected processed experiment profile PA'_m ; wherein for each $m \in \{1, 2, ..., M\}$, said processed experiment profile PA_m comprises a first processed data set, said processed reference profile PC_m comprises a second processed data set, said average processed reference profile $\overline{PC}$ comprises data set $\{\overline{PC}(k)\}$, said first error-corrected processed experiment profile PA'_m comprises dataset $\{PA'_m(k)\}$, said experiment profile XA_m comprises data set $\{XA_m(k)\}$, said reference profile XC_m comprises data set $\{XC_m(k)\}$, wherein said data set $\{XA_m(k)\}$ comprises measurements of a plurality of different cellular constituents measured in

a sample having been subject to a first condition, said data set $\{XC_m(k)\}$ comprises measurements of said plurality of different cellular constituents measured in a sample having been subject to a second condition, and where k = 1, 2, ..., N; k is an index of measurements of cellular constituents, N being the total number of measurements; and

(e) outputting to a user, a user interface device, a computer readable storage medium, or a local or remote computer system; or displaying: said first error-corrected processed experiment profile PA'_m, said data set$\{PA'_m(k)\}$, a second error-corrected processed experiment profile PA''_m, or a data set $\{PA''_m(k)\}$, wherein said second error-corrected processed experiment profile PA''_m comprises said data set $\{PA''_m(k)\}$obtained by combining said first error-corrected processed experiment profile PA'_m with said processed experiment profile PA_m using a weighing factor $\{w(k)\}$, k = 1 , 2, ..., N, wherein $w(k)$ is a weighing factor for the k'th measurement.

100. **(New)** The computer program product of claim 99, wherein said processing step (a) comprises normalizing each said experiment profile XA_m and reference profile XC_m.

101. **(New)** The computer program product of claim 100, wherein said normalizing is carried out according to the equations:

$$NA_m(k) = \frac{XA_m(k)\cdot\overline{XAC}}{\overline{XA_m}}$$

and

$$NC_m(k) = \frac{XC_m(k)\cdot\overline{XAC}}{\overline{XC_m}}$$

where $\{NA_m(k)\}$ is said first data set of said processed experiment profile PA_m, and $\{NC_m(k)\}$ is said second data set of said processed reference profile PC_m; where $\overline{XA_m}$ is an average of measurements or transformed measurements of said plurality of different cellular constituents of said data set $\{XA_m(k)\}$, and $\overline{XC_m}$ is an average of measurements or transformed measurements of said plurality of different cellular constituents of data set $\{XC_m(k)\}$; and wherein $\overline{XAC}$ is an average calculated according to the equation

$$\overline{XAC} = \frac{1}{2M}\sum_{m=1}^{M}(\overline{XA_m} + \overline{XC_m}).$$

102. (**New**) The computer program product of claim 101, wherein the method further comprises normalizing errors of said experiment profile XA_m and reference profile XC_m according to the equations:

$$\sigma_m^A(k) = \frac{\sigma_m^{XA}(k)\cdot\overline{XAC}}{\overline{XA_m}}$$

and

$$\sigma_m^C(k) = \frac{\sigma_m^{XC}(k)\cdot\overline{XAC}}{\overline{XC_m}}$$

where $\sigma_m^{XA}(k)$ and $\sigma_m^{XC}(k)$ are the standard errors of $XA_m(k)$ and $XC_m(k)$,

respectively, and $\sigma_m^A(k)$ and $\sigma_m^C(k)$ are normalized standard errors of $NA_m(k)$ and $NC_m(k)$, respectively.

103. (**New**) The computer program product of claim 102, wherein the method further comprises normalizing background errors of said experiment profile XA_m and reference profile XC_m according to the equations:

$$bkgstd_m^A(k) = \frac{bkgstd_m^{XA}(k)\cdot\overline{XAC}}{\overline{XA_m}}$$

and

$$bkgstd_m^C(k) = \frac{bkgstd_m^{XC}(k)\cdot\overline{XAC}}{\overline{XC_m}}$$

where $bkgstd_m^{XA}(k)$ and $bkgstd_m^{XC}(k)$ are the standard background errors of $XA_m(k)$ and $XC_m(k)$, respectively, and $bkgstd_m^A(k)$ and $bkgstd_m^C(k)$ are normalized standard background errors of said $NA_m(k)$ and said $NC_m(k)$, respectively.

104. (**New**) The computer program product of claim 102, wherein the method further comprises determining said averages $\overline{XA_m}$ and $\overline{XC_m}$ excluding measurements of said plurality of different cellular constituents having a value among the highest 10% of said measurements or transformed measurements of said plurality of different cellular constituents in said data sets $\{XA_m(k)\}$ and $\{XC_m(k)\}$, respectively.

105. (**New**) The computer program product of claim 99, wherein said processing step (a) comprises:

normalizing each said experiment profile XA_m and reference profile XC_m to generate normalized data set $\{NA_m(k)\}$ and normalized data set $\{NC_m(k)\}$, respectively;

transforming said normalized data set $\{NA_m(k)\}$ to obtain a transformed data set $\{TA_m(k)\}$, where said transformed data set $\{TA_m(k)\}$ is said first data set of said processed experiment profile PA_m; and

transforming said normalized data set $\{NC_m(k)\}$ to obtain a transformed data set $\{TC_m(k)\}$, where said transformed data set $\{TC_m(k)\}$ is said second data set of said processed reference profile PC_m.

106. (**New**) The computer program product of claim 105, wherein said transforming is carried out for an experiment according to the equations

$$TA_m(k) = f(x) = \frac{1n\left[\frac{b^2+2\cdot a^2\cdot NA_m(k)}{a} + 2\cdot\sqrt{c^2+b^2\cdot NA_m(k)+a^2\cdot[NA_m(k)]^2}\right]}{a} + d,$$

for $NA_m(k)>0$

and

$$TC_m(k) = f(x) = \frac{1n\left[\frac{b^2+2\cdot a^2\cdot NC_m(k)}{a} + 2\cdot\sqrt{c^2+b^2\cdot NC_m(k)+a^2\cdot[NC_m(k)]^2}\right]}{a} + d,$$

for $NC_m(k)>0$

where d is described by the equation

$$d = \frac{-1n\left[\frac{b^2}{a}+2\cdot c\right]}{a},$$

and where a is the fractional error coefficient of said experiment, b is the Poisson error coefficient of said experiment, and c is the standard deviation of background noise of said experiment.

107. **(New)** The computer program product of claim 99, wherein said processing step (a) comprises:

normalizing each said experiment profile XA_m and reference profile XC_m to generate normalized data set $\{NA_m(k)\}$ and normalized data set $\{NC_m(k)\}$, respectively;

transforming said normalized data set $\{NA_m(k)\}$ to obtain a transformed data set $\{TA_m(k)\}$;

transforming said normalized data set $\{NC_m(k)\}$ to obtain a transformed data set $\{TC_m(k)\}$; and

removing nonlinearity from each said transformed data sets $\{TA_m(k)\}$ and $\{TC_m(k)\}$, respectively.

108. **(New)** The computer program product of claim 107, wherein said removing nonlinearity is carried out by a method comprising

(a1) calculating an average transformed profile of transformed experiment profiles and transformed reference profiles, wherein each of said transformed

experiment profiles contains a corresponding transformed data set $\{TA_m(k)\}$, and each of said transformed reference profiles contains a corresponding transformed data set $\{TC_m(k)\}$; and

(a2) adjusting each of said transformed experiment profiles based on first differences between each of said transformed experiment profiles and said average transformed profile, and adjusting each of said transformed reference profiles based on second differences between each of said transformed reference profiles and said average transformed profile.

109. **(New)** The computer program product of claim 108, wherein the method further comprises calculating said first differences based on the differences in a first subset of transformed measurements of said plurality of different cellular constituents between each of said transformed experiment profiles and said average transformed profile, and calculating said second differences based on the differences in a second subset of transformed measurements of said plurality of different cellular constituents between each of said transformed reference profiles and said average transformed profile.

110. **(New)** The computer program product of claim 109, wherein each said first subset consists of transformed measurements that are ranked similarly between each of said transformed experiment profiles and said average transformed profile, and each said second subset consists of transformed measurements that are ranked similarly

between each of said transformed reference profiles and said average transformed profile.

111. (**New**) The computer program product of claim 110, wherein said adjusting step (a2) is carried out by a method comprising:

(a2i) binning said first subset into a plurality of bins, each said bin consisting of transformed measurements of said plurality of different cellular constituents in one of said transformed experiment profiles and said average transformed profile having a value in a given range; and binning said second subset into a plurality of bins, each said bin consisting of transformed measurements of said plurality of different cellular constituents in one of said transformed reference profiles and said average transformed profile having a value in a given range;

(a2ii) calculating, in each bin of said plurality of bins, a first mean difference between a feature value of transformed measurements of said plurality of different cellular constituents in said one of said transformed experiment profiles and a feature value of said average transformed profile, and calculating a second mean difference between a feature value of transformed measurements of said plurality of different cellular constituents in said one of said reference profiles and a feature value of the average profile;

(a2iii) determining a first curve of said first mean difference as a first function of values of transformed measurements of said plurality of different cellular constituents for said one of said transformed experiment profiles, wherein said first function is represented by, $nonlinear\_TA_m$, and determining a second curve of said second mean

difference as a second function of values of transformed measurements of said plurality of different cellular constituents for said one of said transformed reference profiles, wherein said second function is represented by *nonlinear_*TC_m; and

(a2iv) computing corrected transformed measurements of said plurality of different cellular constituents in each said transformed data set $\{TA_m(k)\}$, according to the equation:

$$TA_m^{corr}(k) = TA_m(k) - nonlinear\_TA_m(k),$$

and computing corrected transformed measurements of said plurality of different cellular constituents in each said transformed data set $\{TC_m(k)\}$, according to the equation:

$$TC_m^{corr}(k) = TC_m(k) - nonlinear\_TC_m(k),$$

where k = 1, ..., N; and where $\{TA_m^{corr}(k)\}$ is said first processed data set of said processed experiment profile PA_m, and $\{TC_m^{corr}(k)\}$ is said second processed data set of said processed reference profile PC_m.

112. (**New**) The computer program product of claim 111, wherein said processed experiment profile PA_m and said processed reference profile PC_m comprise transformed measurements of said plurality of different cellular constituents from the same experimental reaction.

113. **(New)** The computer program product of claim 112, wherein the method further comprises calculating $\overline{PC}(k)$ according to the equation

$$\overline{PC}(k) = \frac{1}{M} \sum_{m=1}^{M} PC_m(k),$$

wherein $\{PC_m(k)\}$ comprises transformed measurements from said second processed data set $\{TC_m^{corr}(k)\}$ and calculating said differential reference profile according to the equation

$$PC_{diff}(m,k) = PC_m(k) - \overline{PC}(k)$$

and wherein said first error-corrected profile is calculated according to the equation

$$PA'_m(k) = PA_m(k) - PC_{diff}(m,k),$$

wherein $\{PA_m(k)\}$ comprises transformed measurements from said first data set $\{TA_m^{corr}(k)\}$.

114. **(New)** The computer program product of claim 113, wherein the method further comprises

(d) calculating for each processed profile pair $\{PA_m, PC_m\}$, where $m \in \{1, 2, ..., M\}$, a second error-corrected experiment profile PA''_m comprising data set $\{PA''_m(k)\}$ by combining said first error-corrected experiment profile PA'_m with said processed experiment profile PA_m using a weighing factor $\{w(k)\}$, $k = 1,2, ..., N$, wherein $w(k)$ is a weighing factor for the k'th measurement.

115. (**New**) The computer program product of claim 114, wherein said second error-corrected experiment profile PA''_m is calculated according to the equation

$$PA''_m(k) = (1\text{-}w(k)) \cdot PA_m(k) + w(k)PA'_m(k).$$

116. (**New**) The computer program product of claim 115, wherein the method further comprises determining said weighing factor according to the equation

$$w(k) = 1\text{-}e^{-0.5\left[\frac{\overline{PC}(k)}{avg\_bkgstd}\right]^2}$$

where *avg_bkgstd* is an average background standard error.

117. (**New**) The computer program product of claim 116, wherein the method further comprises determining said *avg_ bkgstd* according to the equation

$$avg\_bkgstd = \frac{1}{N}\sum_{k=1}^{N}\left[\frac{1}{M}\sum_{m=1}^{M} bkgstd(m,k)\right]$$

where *bkgstd (m, k)* is background standard error of $PC_m(k)$.

118. (**New**) The computer program product of claim 113, wherein the method further comprises determining errors $\{P\sigma'_m\}$ of said first error-corrected experiment profile $\{PA'_m\}$, wherein said $\{P\sigma'_m\}$ comprises error data set $\{P\sigma'_m(k)\}$.

119. (**New**) The computer program product of claim 118, wherein the method further comprises determining said error data set $\{P\sigma'_m(k)\}$ according to the equation

$$\sigma'_m(k) = \sqrt{P\sigma_m^2(k) = mixed\_P\sigma_m{}^2(k) - 2Cor(k) \cdot P\sigma_m(k) \cdot mixed\_P\sigma_m(k)}$$

where $P\sigma_m(k)$ is the standard error of $A_m(k)$, and determining $mixed\_P\sigma_m(k)$ according to the equation

$$mixed\_P\sigma_m(k) = \frac{P\sigma_m(k) + (M-1) \cdot P\sigma_{ref}(k)}{M}$$

where

$$P\sigma_{ref}(k) = \sqrt{\frac{1}{M-1} \sum_m^M (PC_m(k) - \overline{PC}(k))^2}$$

and where Cor(k) is a correlation coefficient between said processed experiment profile PA_m and said processed reference profile PC_m.

120. **(New)** The computer program product of claim 119, wherein said Cor(k) is determined according to the equation

$$Cor(k) = CorMax \cdot \left[1 - e^{-0.5\left[\frac{\overline{PC}(k)}{avg\_bkgstd}\right]^2}\right]$$

where CorMax is a number between 0 and 1.

121. **(New)** The computer program product of claim 120, wherein the method further comprises determining errors $\{P\sigma''_m\}$ of said second error-corrected experiment profile $\{PA''_m\}$ wherein said $\{P\sigma''_m\}$ comprises error data set $\{P\sigma''_m(k)\}$.

122. **(New)** The computer program product of claim 121, wherein the method

further comprises determining said error data set $\{P\sigma''_m(k)\}$ according to the equation

$$P\sigma''_m(k) = \sqrt{[1 - w(k)] \cdot P\sigma_m^2(k) + w(k) P\sigma'^2_m(k)}$$

where $P\sigma_m(k)$ is the standard error of $PA_m(k)$, and the method further comprises determining $P\sigma'_m(k)$ according to the equation

$$P\sigma'_m(k) =$$

$$\sqrt{P\sigma_m^2(k) + mixed\_P\sigma_m{}^2(k) - 2 \cdot Cor(k) \cdot P\sigma_m(k) \cdot mixed\_P\sigma_m(k)},$$ and

the method further comprises determining $mixed\_P\sigma_m(k)$ according to the equation

$$mixed\_P\sigma_m(k) = \frac{P\sigma_m(k) + (M-1) \cdot P\sigma_{ref}(k)}{M}$$

where

$$P\sigma_{ref}(k) = \sqrt{\frac{1}{M-1} \sum_m^M (PC_m(k) - \overline{PC}(k))^2}$$

and where Cor(k) is a correlation coefficient between said processed experiment profile PA_m and said processed reference profile PC_m.

123. (**New**) The computer program product of claim 122, wherein the method further comprises determining said Cor(k) according to the equation

$$Cor(k) = CorMax \cdot \left[1 - e^{-0.5\left[\frac{\overline{PC}(k)}{avg\_bkgstd}\right]^2}\right]$$

where CorMax is a number between 0 and 1.

124. **(New)** The computer program product of claim 123, wherein each said pair of profiles XA_m and XC_m comprise measurements of said plurality of different cellular constituents from a two-channel microarray experiment.

125. **(New)** The computer program product of claim 124, wherein said reference profiles $\{XC_m\}$, $m = 1, 2, \ldots, M$, are measured with samples labeled with a same label.

126. **(New)** The computer program product of claim 125, wherein at least one of said pairs of profiles $\{XA_m, XC_m\}$ is a virtual profile.

127. **(New)** A computer program product for use in conjunction with a computer having a processor and a memory connected to the processor, said computer program product comprising a computer readable storage medium having a computer program mechanism encoded thereon, wherein said computer program mechanism may be loaded into the memory of said computer and cause said computer to carry out a method for generating at least one error-corrected experiment profile of at least one experiment profile A_m, where $m \in \{1, 2, \ldots, M\}$ in at least one of a plurality of pairs of profiles $\{A_m, C_m\}$, A_m being an experiment profile, C_m being a reference profile, where $m = 1, 2, \ldots, M$, M is the number of pairs of profiles, said method comprising:

adjusting, on a computer, said experiment profile A_m using a differential reference profile calculated between C_m and an average reference profile $\bar{C}$ determined for profile pair $\{A_m, C_m\}$ where $m \in \{1, 2, \ldots, M\}$ to generate a first error-corrected experiment profile A'_m; wherein said average reference profile $\bar{C}$ is an average of reference profiles $\{C_m\}$, $m = 1, 2, \ldots, M$; wherein for each $m \in \{1, 2, \ldots, M\}$, said first error-corrected experiment profile A'_m comprises data set $\{A'_m(k)\}$, said experiment profile A_m comprises data set $\{A_m(k)\}$, said reference profile C_m comprises data set $\{C_m(k)\}$, and said average reference profile $\bar{C}$ comprises data set $\{\bar{C}(k)\}$, wherein said data set $\{A_m(k)\}$ comprises measurements or transformed measurements of a plurality of different cellular constituents measured in a sample having been subject to a first condition, said data set $\{C_m(k)\}$ comprises measurements or transformed measurements of said plurality of different cellular constituents measured in a sample having been subject to a second condition, wherein $k = 1, 2, \ldots, N$; k is an index of measurements or transformed measurements of cellular constituents, N being the total number of measurements; and

outputting to a user, a user interface device, a computer readable storage medium, or a local or remote computer system; or displaying: said first error-corrected experiment profile A'_m, said data set $\{A'_m(k)\}$, a second error-corrected experiment profile A''_m, or a data set $\{A''_m(k)\}$, wherein said second error-corrected experiment profile A''_m comprises said data set $\{A''_m(k)\}$ obtained by combining said

first error-corrected experiment profile A'_m with said experiment profile A_m using a weighing factor $\{w(k)\}$, k = 1, 2, ... , N, wherein *w(k)* is a weighing factor for the *k*'th measurement.

128. (**New**) The computer program product of claim 88, wherein the method further comprises obtaining said transformed measurements of said data set $\{A_m(k)\}$ and said data set $\{C_m(k)\}$ for an experiment according to the equations:

$$A_m(k) = f(x) = \frac{1n\left[\frac{b^2+2\cdot a^2\cdot XA_m(k)}{a}+2\cdot\sqrt{c^2+b^2\cdot XA_m(k)+a^2\cdot[XA_m(k)]^2}\right]}{a} + d,$$

for $XA_m(k)>0$

and

$$C_m(k) = f(x) = \frac{1n\left[\frac{b^2+2\cdot a^2\cdot XC_m(k)}{a}+2\cdot\sqrt{c^2+b^2\cdot XC_m(k)+a^2\cdot[XC_m(k)]^2}\right]}{a} + d,$$

for $XC_m(k)>0$

where $\{XA_m(k)\}$ and $\{XC_m(k)\}$ are data sets comprising measurements of said plurality of different cellular constituents that when transformed produce said transformed measurements of said plurality of different cellular constituents of said data set $A_m(k)$ and said data set $C_m(k)$, respectively, where *d* is described by the equation:

$$d = \frac{-1n\left[\frac{b^2}{a}+2\cdot c\right]}{a}$$

and where *a* is the fractional error coefficient of said experiment, *b* is the Poisson

error coefficient of said experiment, and *c* is the standard deviation of background noise of said experiment.

129. **(New)** The computer program product of claim 99, wherein said processing comprises:

normalizing, transforming, and/or removing nonlinearity from measurements of said plurality of cellular constituents of said data set $\{XA_m(k)\}$ of said experiment profile XA_m, and from measurements of said plurality of cellular constituents of said data set $\{XC_m(k)\}$ of said reference profile XC_m.

130. **(New)** A computer system comprising:

a processor; and

a memory coupled to said processor and encoding one or more programs;

wherein said one or more programs cause the processor to carry out a method for generating at least one error-corrected experiment profile of at least one experiment profile in a plurality of pairs of profiles $\{A_m,C_m\}$, where $m = 1, 2, \ldots, M$, and M is the number of the pairs of profiles; and wherein, for each $m \in \{1, 2, \ldots, M\}$, A_m is an experiment profile, and C_m is a reference profile; and wherein $\{A_m\}$ represents experiment profiles in said plurality of pairs of profiles $\{A_m,C_m\}$ and $\{C_m\}$ represents reference profiles in said plurality of pairs of profiles $\{A_m, C_m\}$, said method comprising:

(a) calculating, on a computer, an average reference profile $\bar{C}$ of said plurality of

reference profiles $\{C_m\}$ where m = 1, 2, …, M;

(b) determining, on a computer, for at least one profile pair $\{A_m,C_m\}$where $m \in \{1, 2, \ldots, M\}$ of said plurality of pairs of profiles $\{A_m, C_{m,}\}$ a differential reference profile computed between C_m and $\bar{C}$;

(c) adjusting, on a computer, an experiment profile A_m of said at least one profile pair $\{A_m, C_m\}$ where $m \in \{1, 2, \ldots, M\}$ based on said differential reference profile determined for said profile pair to generate a first error-corrected experiment profile A'_m for each $m \in \{1, 2, \ldots, M\}$, wherein said experiment profile A_m comprises a first data set, said reference profile C_m comprises a second data set, said average reference profile $\bar{C}$ comprises data set $\{\bar{C}\ (k)\}$, and said first error-corrected experiment profile A'_m comprises data set $\{A'_m\ (k)\}$; wherein said first data set comprises measurements or transformed measurements of a plurality of different cellular constituents measured in a sample having been subject to a first condition, said second data set comprises measurements or transformed measurements of said plurality of different cellular constituents measured in a sample having been subject to a second condition; and wherein k = 1, 2, ..., N; k is an index of measurements or transformed measurements of said plurality of different cellular constituents, N being the total number of measurements or transformed measurements; and

(d) outputting to a user, a user interface device, a computer readable storage medium, or a local or remote computer system; or displaying: said first error-corrected experiment profile A'_m, said data set $\{A'_m(k)\}$, a second error-corrected experiment

profile A''_m, or a data set $\{A''_m(k)\}$, wherein said second error-corrected experiment profile A''_m comprises said data set $\{A''_m(k)\}$ obtained by combining said first error-corrected experiment profile A'_m with said experiment profile A_m using a weighing factor $\{w(k)\}$, k = 1, 2, ... , N, wherein $w(k)$ is a weighing factor for the k'th measurement.

131. (**New**) The computer system of claim 130, wherein said steps (b) and (c) are performed for each profile pair $\{A_m, C_m\}$ where $m \in \{1, 2, \ldots, M\}$.

132. (**New**) The computer system of claim 131, wherein each of said experiment profile A_m and said reference profile C_m comprises measurements or transformed measurements of said plurality of different cellular constituents from the same experimental reaction.

133. (**New**) The computer system of claim 132, wherein said $\bar{C}(k)$ is calculated according to the equation

$$\bar{C}(k) = \frac{1}{M}\sum_{m=1}^{M} C_m(k)$$

wherein said differential reference profile is determined according to the equation

$$C_{diff}(m,k) = C_m(k) - \bar{C}(k)$$

and wherein said first error-corrected experiment profile A'_m is generated according to the equation

$$A'_m(k) = A_m(k) - C_{diff}(m, k)$$

wherein $\{A_m(k)\}$ is said first data set of experiment profile A_m.

134. **(New)** The computer system of claim 133, wherein the method further comprises:

(d) calculating, for each said profile pair $\{A_m, C_m\}$ said second error-corrected experiment profile A''_m; and

(e) outputting to, a user interface device, a computer readable storage medium, or a local or remote computer system; or displaying; said second error-corrected experiment profile A''_m or said data set $\{A''_m(k)\}$.

135. **(New)** The computer system of claim 134, wherein said second error-corrected experiment profile A''_m is calculated according to the equation

$$A''_m(k) = (1-w(k)) \cdot A_m(k) + w(k) \cdot A'_m(k).$$

136. **(New)** The computer system of claim 135, wherein the method further comprises determining said weighing factor *w(k)* according to the equation

$$w(k) = 1 - e^{-0.5\left[\frac{\bar{C}(k)}{avg\_bkgstd}\right]^2}$$

where *avg_bkgstd* is an average background standard error.

137. (**New**) The computer system of claim 136, wherein the method further comprises determining said *avg_bkgstd* according to the equation

$$avg\_bkgstd = \frac{1}{N}\sum_{k=1}^{N}\left[\frac{1}{M}\sum_{m=1}^{M} bkgstd(m,k)\right]$$

where *bkgstd (m, k)* is background standard error of $C_m(k)$.

138. (**New**) The computer system of claim 133, wherein the method further comprises determining errors $\{\sigma'_m(k)\}$ of said data set $\{A'_m(k)\}$ in said first error-corrected experiment profile A'_m.

139. (**New**) The computer system of claim 138, wherein the method further comprises determining said errors $\{\sigma'_m(k)\}$ according to the equation

$$\sigma'_m(k) = \sqrt{\sigma_m^2(k) + mixed\_\sigma_m^2(k) - 2 \cdot Cor(k) \cdot \sigma_m(k) \cdot mixed\_\sigma_m(k)}$$

where σ_m *(k)* is the standard error of $A_m(k)$, the method further comprising determining *mixed* _ σ_m *(k)* according to the equation

$$mixed\_\sigma_m(k) = \frac{\sigma_m(k) + (M-1) \cdot \sigma_{ref}(k)}{M}$$

where $\sigma_{ref}(k) = \sqrt{\frac{1}{M-1}\sum_{m}^{M} (C_m(k) - \bar{C}(k))^2}$

and where Cor(k) is a correlation coefficient between said experiment profile A_m

and said reference profile C_m.

140. (**New**) The computer system of claim 139, wherein the method further comprises determining said Cor(k) according to the equation

$$Cor(k) = CorMax \cdot \left[1 - e^{-0.5 \cdot \left[\frac{\bar{C}(k)}{avg\_bkgstd}\right]^2}\right]$$

where CorMax is a number between 0 and 1.

141. (**New**) The computer system of claim 136, wherein the method further comprises determining errors $\{\sigma"_m(k)\}$ of said data set $\{A"_m(k)\}$ in said second error-corrected experiment profile A''_m.

142. (**New**) The computer system of claim 141, wherein said errors $\{\sigma"_m(k)\}$ are determined according to the equation

$$\sigma"_m(k) = \sqrt{[1 - w(k)] \cdot \sigma_m^2(k) + w(k)\sigma'_m{}^2(k)}$$

where $\sigma_m(k)$ is the standard error of $A_m(k)$, the method further comprising (i) determining $\sigma'_m(k)$ according to the equation

$$\sigma'_m(k) = \sqrt{\sigma_m^2(k) + mixed\_\sigma_m{}^2(k) - 2 \cdot Cor(k) \cdot \sigma_m(k) \cdot mixed\_\sigma_m(k)},$$ and

(ii) determining $mixed\_\sigma_m(k)$ according to the equation

$$mixed\_\sigma_m(k) = \frac{\sigma_m(k) + (M-1)\cdot\sigma_{ref}(k)}{M}$$

where $\sigma_{ref}(k) = \sqrt{\frac{1}{M-1}\sum_{m}^{M}(c_m(k) - \bar{C}(k))^2}$

and where Cor(k) is a correlation coefficient between said experiment profile A_m and said reference profile C_m.

143. **(New)** The computer system of claim 142, wherein the method further comprises determining said Cor(k) according to the equation

$$Cor(k) = CorMax \cdot \left[1 - e^{-0.5\cdot\left[\frac{\bar{C}(k)}{avg\_bkgstd}\right]^2}\right]$$

where CorMax is a number between 0 and 1.

144. **(New)** The computer system of claim 131, wherein said experiment profile A_m and said reference profile C_m of each said profile pair $\{A_m, C_m\}$ are measured in a two-channel microarray experiment.

145. **(New)** The computer system of claim 144, wherein said reference profiles $\{C_m\}$, where m = 1, 2, ... , M, are measured with samples labeled with a same label.

146. **(New)** The computer system of claim 131, wherein at least one of said plurality of pairs of profiles $\{A_m, C_m\}$ is a virtual profile.

147. **(New)** The computer system of claim 130, wherein said plurality of pairs of profiles $\{A_m, C_m\}$ are transformed profiles each comprising transformed measurements of said plurality of different cellular constituents in data set $\{A_m(k)\}$ and data set $\{C_m(k)\}$, respectively; and wherein said data set $\{A_m(k)\}$ is said first data set, and said data set $\{C_m(k)\}$ is said second data set.

148. **(New)** The computer system of claim 130, wherein the method further comprises:

(a0) removing nonlinearity, prior to said calculating step (a), from measurements or transformed measurements of said plurality of different cellular constituents to generate said plurality of pairs of profiles $\{A_m, C_m\}$ comprising said experiment profile A_m and reference profile C_m.

149. **(New)** The computer system of claim 148, wherein said removing step (a0) comprises:

(a0i) calculating an average profile of pre-experiment profiles $\{A_m^{pre}\}$ and pre- reference profiles $\{C_m^{pre}\}$; wherein each of said pre-experiment profiles comprises measurements or transformed measurements of said plurality of different cellular constituents measured in said sample having been subject to said first

condition, which when nonlinearity is removed therefrom, produces each said experiment profile A_m; and wherein each of said pre-reference profiles comprises measurements or transformed measurements of said plurality of different cellular constituents measured in said sample having been subject to said second condition, which when nonlinearity is removed therefrom, produces each said reference profile C_m; and

(a0ii) adjusting each of said pre-experiment profiles $\{A_m^{pre}\}$ based on first differences between each of said pre-experiment profiles $\{A_m^{pre}\}$ and said average profile, thereby generating each said experiment profile A_m; and adjusting each of pre-reference profiles $\{C_m^{pre}\}$ based on second differences between each of said pre-reference profiles $\{C_m^{pre}\}$ and said average profile, thereby generating each said reference profile C_m.

150. **(New)** The computer system of claim 149, wherein the method further comprises calculating said first differences based on a first subset of said measurements or transformed measurements of said plurality of different cellular constituents in said pre-experiment profiles $\{A_m^{pre}\}$ and said average profile; and calculating said second differences based on a second subset of said measurements or transformed measurements of said plurality of different cellular constituents in said pre-reference profiles $\{C_m^{pre}\}$ and said average profile.

151. **(New)** The computer system of claim 150, wherein said first subset consists of measurements or transformed measurements of said plurality of different cellular constituents that are ranked similarly between each of said pre-experiment profiles $\{A_m^{pre}\}$ and said average profile, and said second subset consists of measurements or transformed measurements of said plurality of different cellular constituents that are ranked similarly between each of said pre-reference profiles $\{C_m^{pre}\}$ and said average profile.

152. **(New)** The computer system of claim 151, wherein said adjusting step (a0ii) is carried out by a method comprising:

(ii1) binning said first subset into a first plurality of bins, wherein each of said first plurality of bins consists of measurements or transformed measurements of said plurality of different cellular constituents in one of said pre-experiment profiles $\{A_m^{pre}\}$ and said average profile having a value in a given range; and binning said second subset into a second plurality of bins, wherein each of said second plurality of bins consists of measurements or transformed measurements of said plurality of different cellular constituents in one of said pre-reference profiles $\{C_m^{pre}\}$and said average profile having a value in a given range;

(ii2) calculating, in each bin of said first plurality of bins, a first mean difference between a feature value of measurements or transformed measurements

of said one of said pre-experiment profiles $\{A_m^{pre}\}$ and a feature value of said average profile, and calculating a second mean difference between a feature value of measurements or transformed measurements of said one of said pre-reference profiles $\{C_m^{pre}\}$ and a feature value of said average profile;

(ii3) determining a first curve of said first mean difference as a first function of values of measurements or transformed measurements of said plurality of different cellular constituents for said one of said pre-experiment profiles $\{A_m^{pre}\}$,wherein said first function is represented by, $nonlinear\_A_m^{pre}$; and determining a second curve of said second mean difference as a second function of values of measurements or transformed measurements of said plurality of different cellular constituents for said one of said pre-reference profiles $\{C_m^{pre}\}$,wherein said second function is represented by $nonlinear\_C_m^{pre}$; and

(ii4) adjusting each of said pre-experiment profiles $\{A_m^{pre}\}$ according to the equation:

$$A_m(k) = A_m^{pre}(k) - nonlinear\_A_m^{pre}(k),$$

and adjusting each of said pre-reference profiles $\{C_m^{pre}\}$ according to the equation:

$$C_m(k) = C_m^{pre}(k) - nonlinear\_C_m^{pre}(k),$$

where k = 1, ... , N; and where $A_m^{pre}(k)$ and $C_m^{pre}(k)$ are data sets of each of said

pre-experiment profiles $\{A_m^{pre}\}$ and each of said pre-reference profiles $\{C_m^{pre}\}$, respectively; and where $A_m(k)$ and $C_m(k)$ are said first data set and said second data set, respectively.

153. (**New**) The computer system of claim 130, wherein the method further comprises:

(a0) normalizing, prior to said calculating step (a), measurements or transformed measurements of said plurality of different cellular constituents in a pre-experiment profile A_m^{pre} and a pre-reference profile C_m^{pre} to generate said experiment profile A_m and said reference profile C_m, respectively.

154. (**New**) The computer system of claim 153, wherein said normalizing step (a0) comprises normalizing a data set $A_m^{pre}(k)$ and a data set $C_m^{pre}(k)$, according to the equations:

$$A_m(k) = \frac{A_m^{pre}(k) \cdot \overline{A_m^{pre} C_m^{pre}}}{\overline{A_m^{pre}}}$$

and

$$C_m(k) = \frac{C_m^{pre}(k) \cdot \overline{A_m^{pre} C_m^{pre}}}{\overline{C_m^{pre}}},$$

wherein said data sets $A_m^{pre}(k)$ and $C_m^{pre}(k)$ each comprises measurements or transformed measurements of said plurality of different cellular constituents, where

$\overline{A_m^{pre}}$ is an average of measurements or transformed measurements of said plurality of different cellular constituents in said $A_m^{pre}(k)$, and $\overline{C_m^{pre}}$ is an average of measurements or transformed measurements of said plurality of different cellular constituents in said $C_m^{pre}(k)$, wherein $A_m(k)$ is said first data set, wherein $A_m(k)$ comprises normalized measurements or normalized transformed measurements of said pre-experiment profile A_m^{pre}; and $C_m(k)$ is said second data set wherein $A_m(k)$ comprises normalized measurements or normalized transformed measurements of said reference profile C_m^{pre}; and wherein $\overline{A_m^{pre} C_m^{pre}}$ is an average calculated according to the equation

$$\overline{A_m^{pre} C_m^{pre}} = \frac{1}{2M} \sum_{m=1}^{M} (\overline{A_m^{pre}} + \overline{C_m^{pre}}).$$

155. (**New**) The computer system of claim 154, wherein the method further comprises normalizing errors of said data sets { A_m^{pre} (k) } and { C_m^{pre} (k) }, respectively, according to the equations:

$$\sigma_m^{NA}(k) = \frac{\sigma_m^{preA}(k) \cdot \overline{A_m^{pre} C_m^{pre}}}{\overline{A_m^{pre}}}$$

and

$$\sigma_m^{NC}(k) = \frac{\sigma_m^{preC}(k) \cdot \overline{A_m^{pre} C_m^{pre}}}{\overline{C_m^{pre}}},$$

where $\sigma_m^{preA}(k)$ and $\sigma_m^{preC}(k)$ are the standard errors of $A_m^{pre}(k)$ and $C_m^{pre}(k)$, respectively, and $\sigma_m^{NA}(k)$ and $\sigma_m^{NC}(k)$ are normalized standard errors of $A_m(k)$ and $C_m(k)$, respectively.

156. **(New)** The computer system of claim 155, wherein the method further comprises normalizing background errors of said data sets $\{A_m^{pre}(k)\}$ and $\{C_m^{pre}(k)\}$, respectively, according to the equations:

$$bkgstd_m^{NA}(k) = \frac{bkgstd_m^{preA}(k) \cdot \overline{A_m^{pre} C_m^{pre}}}{\overline{A_m^{pre}}}$$

and

$$bkgstd_m^{NC}(k) = \frac{bkgstd_m^{preC}(k) \cdot \overline{A_m^{pre} C_m^{pre}}}{\overline{C_m^{pre}}}$$

where $bkgstd_m^{preA}(k)$ and $bkgstd_m^{preC}(k)$ are the standard background errors of $A_m^{pre}(k)$ and $C_m^{pre}(k)$, respectively, and $bkgstd_m^{NA}(k)$ and $bkgstd_m^{NC}(k)$ are normalized standard background errors of $A_m(k)$ and $C_m(k)$, respectively.

157. **(New)** The computer system of claim 156, wherein the method further comprises calculating said averages $\overline{A_m^{pre}}$ and $\overline{C_m^{pre}}$ by excluding measurements or transformed measurements of said plurality of different cellular constituents having a value among the highest 10% of said measurements or transformed measurements

of said plurality of different cellular constituents in said data sets $\{A_m^{pre}(k)\}$ and $\{C_m^{pre}(k)\}$, respectively.

158. **(New)** A computer system comprising:

a processor; and

a memory coupled to said processor and encoding one or more programs;

wherein said one or more programs cause the processor to carry out a method for generating at least one error-corrected experiment profile of at least one experiment profile in a plurality of pairs of profiles $\{XA_m, XC_m\}$, XA_m being an experiment profile, XC_m being a reference profile, where m = 1, 2, ... , M, M is the number of pairs of profiles, said method comprising:

(a) processing, on a computer, said plurality of pairs of profiles $\{XA_m, XC_m\}$ to obtain a plurality of pairs of processed profiles $\{PA_m, PC_m\}$, PA_m being a processed experiment profile, PC_m being a processed reference profile;

(b) calculating, on a computer, an average processed reference profile $\overline{PC}$ of processed reference profiles $\{PC_m\}$, where m = 1,2, ..., M;

(c) determining, on a computer, for at least one processed profile pair $\{PA_m, PC_m\}$ where $m \in \{1, 2, ..., M\}$ of said plurality of pairs of processed profiles $\{PA_m, PC_m\}$, where m = 1, 2, ..., M, a differential reference profile computed between PC_m and $\overline{PC}$;

(d) adjusting, on a computer, a processed experiment profile PA_m of said at

least one processed profile pair $\{PA_m, PC_m\}$ where $m \in \{1, 2, ..., M\}$ using said differential reference profile determined for said at least one processed profile pair to generate a first error-corrected processed experiment profile PA'_m ; wherein for each $m \in \{1, 2, ..., M\}$, said processed experiment profile PA_m comprises a first processed data set, said processed reference profile PC_m comprises a second processed data set, said average processed reference profile $\overline{PC}$ comprises data set $\{\overline{PC}(k)\}$, said first error-corrected processed experiment profile PA'_m comprises dataset $\{PA'_m(k)\}$, said experiment profile XA_m comprises data set $\{XA_m(k)\}$, said reference profile XC_m comprises data set $\{XC_m(k)\}$, wherein said data set $\{XA_m(k)\}$ comprises measurements of a plurality of different cellular constituents measured in a sample having been subject to a first condition, said data set $\{XC_m(k)\}$ comprises measurements of said plurality of different cellular constituents measured in a sample having been subject to a second condition, and where $k = 1, 2, ..., N$; k is an index of measurements of cellular constituents, N being the total number of measurements; and

(e) outputting to a user, a user interface device, a computer readable storage medium, or a local or remote computer system; or displaying: said first error-corrected processed experiment profile PA'_m, said data set$\{PA'_m(k)\}$, a second error-corrected processed experiment profile PA''_m, or a data set $\{PA''_m(k)\}$, wherein said second error-corrected processed experiment profile PA''_m comprises said data set $\{PA''_m(k)\}$obtained by combining said first error-corrected processed experiment profile PA'_m with said processed experiment profile PA_m using a weighing factor

$\{w(k)\}$, k = 1 , 2, ..., N, wherein $w(k)$ is a weighing factor for the k'th measurement.

159. **(New)** The computer system of claim 158, wherein said processing step (a) comprises normalizing each said experiment profile XA_m and reference profile XC_m.

160. **(New)** The computer system of claim 159, wherein said normalizing is carried out according to the equations:

$$NA_m(k) = \frac{XA_m(k) \cdot \overline{XAC}}{\overline{XA_m}}$$

and

$$NC_m(k) = \frac{XC_m(k) \cdot \overline{XAC}}{\overline{XC_m}}$$

where $\{NA_m(k)\}$ is said first data set of said processed experiment profile PA_m, and $\{NC_m(k)\}$ is said second data set of said processed reference profile PC_m; where $\overline{XA_m}$ is an average of measurements or transformed measurements of said plurality of different cellular constituents of said data set $\{XA_m(k)\}$, and $\overline{XC_m}$ is an average of measurements or transformed measurements of said plurality of different cellular constituents of data set $\{XC_m(k)\}$; and wherein $\overline{XAC}$ is an average calculated according to the equation

$$\overline{XAC} = \frac{1}{2M} \sum_{m=1}^{M} (\overline{XA_m} + \overline{XC_m}).$$

161. (**New**) The computer system of claim 160, wherein the method further comprises normalizing errors of said experiment profile XA_m and reference profile XC_m according to the equations:

$$\sigma_m^A(k) = \frac{\sigma_m^{XA}(k) \cdot \overline{XAC}}{\overline{XA_m}}$$

and

$$\sigma_m^C(k) = \frac{\sigma_m^{XC}(k) \cdot \overline{XAC}}{\overline{XC_m}}$$

where $\sigma_m^{XA}(k)$ and $\sigma_m^{XC}(k)$ are the standard errors of $XA_m(k)$ and $XC_m(k)$, respectively, and $\sigma_m^A(k)$and $\sigma_m^C(k)$ are normalized standard errors of $NA_m(k)$ and $NC_m(k)$, respectively.

162. (**New**) The computer system of claim 161, wherein the method further comprises normalizing background errors of said experiment profile XA_m and reference profile XC_m according to the equations:

$$bkgstd_m^A(k) = \frac{bkgstd_m^{XA}(k) \cdot \overline{XAC}}{\overline{XA_m}}$$

and

$$bkgstd_m^C(k) = \frac{bkgstd_m^{XC}(k) \cdot \overline{XAC}}{\overline{XC_m}}$$

where $bkgstd^{XA}_{m}(k)$ and $bkgstd^{XC}_{m}(k)$ are the standard background errors of $XA_m(k)$ and $XC_m(k)$, respectively, and $bkgstd^{A}_{m}(k)$ and $bkgstd^{C}_{m}(k)$ are normalized standard background errors of said $NA_m(k)$ and said $NC_m(k)$, respectively.

163. (**New**) The computer system of claim 161, wherein the method further comprises determining said averages $\overline{XA_m}$ and $\overline{XC_m}$ excluding measurements of said plurality of different cellular constituents having a value among the highest 10% of said measurements or transformed measurements of said plurality of different cellular constituents in said data sets $\{XA_m(k)\}$ and $\{XC_m(k)\}$, respectively.

164. (**New**) The computer system of claim 158, wherein said processing step (a) comprises:

normalizing each said experiment profile XA_m and reference profile XC_m to generate normalized data set $\{NA_m(k)\}$ and normalized data set $\{NC_m(k)\}$, respectively;

transforming said normalized data set $\{NA_m(k)\}$ to obtain a transformed data set $\{TA_m(k)\}$, where said transformed data set $\{TA_m(k)\}$ is said first data set of said processed experiment profile PA_m; and

transforming said normalized data set $\{NC_m(k)\}$ to obtain a transformed data set $\{TC_m(k)\}$, where said transformed data set $\{TC_m(k)\}$ is said second data set of said processed reference profile PC_m.

165. **(New)** The computer system of claim 164, wherein said transforming is carried out for an experiment according to the equations

$$TA_m(k) = f(x) = \frac{1n\left[\frac{b^2+2\cdot a^2\cdot NA_m(k)}{a} + 2\cdot\sqrt{c^2+b^2\cdot NA_m(k)+a^2\cdot[NA_m(k)]^2}\right]}{a} + d,$$

for $NA_m(k)>0$

and

$$TC_m(k) = f(x) = \frac{1n\left[\frac{b^2+2\cdot a^2\cdot NC_m(k)}{a} + 2\cdot\sqrt{c^2+b^2\cdot NC_m(k)+ a^2\cdot[NC_m(k)]^2}\right]}{a} + d,$$

for $NC_m(k)>0$

where d is described by the equation

$$d = \frac{-1n\left[\frac{b^2}{a}+2\cdot c\right]}{a}$$

and where a is the fractional error coefficient of said experiment, b is the Poisson error coefficient of said experiment, and c is the standard deviation of background noise of said experiment.

166. **(New)** The computer system of claim 158, wherein said processing step (a) comprises:

normalizing each said experiment profile XA_m and reference profile XC_m to generate normalized data set $\{NA_m(k)\}$ and normalized data set $\{NC_m(k)\}$, respectively;

transforming said normalized data set $\{NA_m(k)\}$ to obtain a transformed data set $\{TA_m(k)\}$;

transforming said normalized data set $\{NC_m(k)\}$ to obtain a transformed data set $\{TC_m(k)\}$; and

removing nonlinearity from each said transformed data sets $\{TA_m(k)\}$ and $\{TC_m(k)\}$, respectively.

167. **(New)** The computer system of claim 166, wherein said removing nonlinearity is carried out by a method comprising

(a1) calculating an average transformed profile of transformed experiment profiles and transformed reference profiles, wherein each of said transformed experiment profiles contains a corresponding transformed data set $\{TA_m(k)\}$, and each of said transformed reference profiles contains a corresponding transformed data set $\{TC_m(k)\}$; and

(a2) adjusting each of said transformed experiment profiles based on first differences between each of said transformed experiment profiles and said average transformed profile, and adjusting each of said transformed reference profiles based on second differences between each of said transformed reference profiles and said average transformed profile.

168. **(New)** The computer system of claim 167, wherein the method further comprises calculating said first differences based on the differences in a first subset of transformed measurements of said plurality of different cellular constituents between each of said transformed experiment profiles and said average transformed

profile, and calculating said second differences based on the differences in a second subset of transformed measurements of said plurality of different cellular constituents between each of said transformed reference profiles and said average transformed profile.

169. **(New)** The computer system of claim 168, wherein each said first subset consists of transformed measurements that are ranked similarly between each of said transformed experiment profiles and said average transformed profile, and each said second subset consists of transformed measurements that are ranked similarly between each of said transformed reference profiles and said average transformed profile.

170. **(New)** The computer system of claim 169, wherein said adjusting step (a2) is carried out by a method comprising:

(a2i) binning said first subset into a plurality of bins, each said bin consisting of transformed measurements of said plurality of different cellular constituents in one of said transformed experiment profiles and said average transformed profile having a value in a given range; and binning said second subset into a plurality of bins, each said bin consisting of transformed measurements of said plurality of different cellular constituents in one of said transformed reference profiles and said average transformed profile having a value in a given range;

(a2ii) calculating, in each bin of said plurality of bins, a first mean difference between a feature value of transformed measurements of said plurality of different cellular constituents in said one of said transformed experiment profiles and a feature

value of said average transformed profile, and calculating a second mean difference between a feature value of transformed measurements of said plurality of different cellular constituents in said one of said reference profiles and a feature value of the average profile;

(a2iii) determining a first curve of said first mean difference as a first function of values of transformed measurements of said plurality of different cellular constituents for said one of said transformed experiment profiles, wherein said first function is represented by, $nonlinear\_TA_m$, and determining a second curve of said second mean difference as a second function of values of transformed measurements of said plurality of different cellular constituents for said one of said transformed reference profiles, wherein said second function is represented by $nonlinear\_TC_m$; and

(a2iv) computing corrected transformed measurements of said plurality of different cellular constituents in each said transformed data set $\{TA_m(k)\}$, according to the equation:

$$TA_m^{corr}(k) = TA_m(k) - nonlinear\_TA_m(k),$$

and computing corrected transformed measurements of said plurality of different cellular constituents in each said transformed data set $\{TC_m(k)\}$, according to the equation:

$$TC_m^{corr}(k) = TC_m(k) - nonlinear\_TC_m(k),$$

where k = 1, ..., N; and where $\{TA_m^{corr}(k)\}$ is said first processed data set of said

processed experiment profile PA_m, and $\{TC_m^{corr}(k)\}$ is said second processed data set of said processed reference profile PC_m.

171. (**New**) The computer system of claim 170, wherein said processed experiment profile PA_m and said processed reference profile PC_m comprise transformed measurements of said plurality of different cellular constituents from the same experimental reaction.

172. (**New**) The computer system of claim 171, wherein the method further comprises calculating $\overline{PC}(k)$ according to the equation

$$\overline{PC}(k) = \frac{1}{M} \sum_{m=1}^{M} PC_m(k),$$

wherein $\{PC_m(k)\}$ comprises transformed measurements from said second processed data set $\{TC_m^{corr}(k)\}$ and calculating said differential reference profile according to the equation

$$PC_{diff}(m,k) = PC_m(k) - \overline{PC}(k)$$

and wherein said first error-corrected profile is calculated according to the equation

$$PA'_m(k) = PA_m(k) - PC_{diff}(m,k),$$

wherein $\{ PA_m (k) \}$comprises transformed measurements from said first data set $\{TA_m^{corr}(k)\}$.

173. (**New**) The computer system of claim 172, wherein the method further comprises

(d) calculating for each processed profile pair $\{PA_m, PC_m\}$, where $m \in \{1, 2, ..., M\}$, a second error-corrected experiment profile PA''_m comprising data set $\{PA''_m(k)\}$ by combining said first error-corrected experiment profile PA'_m with said processed experiment profile PA_m using a weighing factor $\{w(k)\}$, $k = 1,2, ..., N$, wherein $w(k)$ is a weighing factor for the k'th measurement.

174. (**New**) The computer system of claim 173, wherein said second error-corrected experiment profile PA''_m is calculated according to the equation

$$PA''_m(k) = (1-w(k)) \cdot PA_m(k) + w(k)PA'_m(k).$$

175. (**New**) The computer system of claim 174, wherein the method further comprises determining said weighing factor according to the equation

$$w(k) = 1-e^{-0.5\left[\frac{\overline{PC}(k)}{avg\_bkgstd}\right]^2}$$

where *avg_bkgstd* is an average background standard error.

176. (**New**) The computer system of claim 175, wherein the method further comprises determining said *avg_ bkgstd* according to the equation

$$avg\_bkgstd = \frac{1}{N}\sum_{k=1}^{N}\left[\frac{1}{M}\sum_{m=1}^{M} bkgstd(m,k)\right]$$

where *bkgstd (m, k)* is background standard error of $PC_m(k)$.

177. (**New**) The computer system of claim 172, wherein the method further comprises determining errors $\{P\sigma'_m\}$ of said first error-corrected experiment profile $\{PA'_m\}$, wherein said $\{P\sigma'_m\}$ comprises error data set $\{P\sigma'_m(k)\}$.

178. (**New**) The computer system of claim 177, wherein the method further comprises determining said error data set $\{P\sigma'_m(k)\}$ according to the equation

$$\sigma'_m(k) = \sqrt{P\sigma_m^2(k) = mixed\_P\sigma_m{}^2(k) - 2Cor(k)\cdot P\sigma_m(k)\cdot mixed\_P\sigma_m(k)}$$

where $P\sigma_m(k)$ is the standard error of $A_m(k)$, and determining $mixed\_P\sigma_m(k)$ according to the equation

$$mixed\_P\sigma_m(k) = \frac{P\sigma_m(k) + (M-1)\cdot P\sigma_{ref}(k)}{M}$$

where

$$P\sigma_{ref}(k) = \sqrt{\frac{1}{M-1}\sum_{m}^{M}\left(PC_m(k) - \overline{PC}(k)\right)^2}$$

and where Cor(k) is a correlation coefficient between said processed experiment profile PA_m and said processed reference profile PC_m.

179. (**New**) The computer system of claim 178, wherein said Cor(k) is determined according to the equation

$$Cor(k) = CorMax \cdot \left[1 - e^{-0.5\left[\frac{\overline{PC}(k)}{avg\_bkgstd}\right]^2}\right]$$

where CorMax is a number between 0 and 1.

180. **(New)** The computer system of claim 179, wherein the method further comprises determining errors $\{P\sigma''_m\}$ of said second error-corrected experiment profile $\{PA''_m\}$wherein said $\{P\sigma''_m\}$ comprises error data set $\{P\sigma''_m(k)\}$.

181. **(New)** The computer system of claim 180, wherein the method further comprises determining said error data set $\{P\sigma''_m(k)\}$ according to the equation

$$P\sigma''_m(k) = \sqrt{[1 - w(k)] \cdot P\sigma_m^2(k) + w(k)P\sigma'^2_m(k)}$$

where $P\sigma_m(k)$ is the standard error of $PA_m(k)$, and the method further comprises determining $P\sigma'_m(k)$ according to the equation

$$P\sigma'_m(k) =$$

$$\sqrt{P\sigma_m^2(k) + mixed\_P\sigma_m{}^2(k) - 2 \cdot Cor(k) \cdot P\sigma_m(k) \cdot mixed\_P\sigma_m(k)},$$ and

the method further comprises determining $mixed\_P\sigma_m(k)$ according to the equation

$$mixed\_P\sigma_m(k) = \frac{P\sigma_m(k) + (M-1) \cdot P\sigma_{ref}(k)}{M}$$

where

$$P\sigma_{ref}(k) = \sqrt{\frac{1}{M-1} \sum_m^M (PC_m(k) - \overline{PC}(k))^2}$$

and where Cor(k) is a correlation coefficient between said processed experiment profile PA_m and said processed reference profile PC_m.

182. **(New)** The computer system of claim 181, wherein the method further comprises determining said Cor(k) according to the equation

$$Cor(k) = CorMax \cdot \left[1 - e^{-0.5\left[\frac{\overline{PC}(k)}{avg\_bkgstd}\right]^2}\right]$$

where CorMax is a number between 0 and 1.

183. **(New)** The computer system of claim 182, wherein each said pair of profiles XA_m and XC_m comprise measurements of said plurality of different cellular constituents from a two-channel microarray experiment.

184. **(New)** The computer system of claim 183, wherein said reference profiles $\{XC_m\}$, m = 1, 2, ... , M, are measured with samples labeled with a same label.

185. **(New)** The computer system of claim 184, wherein at least one of said pairs of profiles $\{XA_m, XC_m\}$ is a virtual profile.

186. **(New)** A computer system comprising:

a processor; and

a memory coupled to said processor and encoding one or more programs;

wherein said one or more programs cause the processor to carry out a method

for generating at least one error-corrected experiment profile of at least one experiment profile A_m, where $m \in \{1, 2, ..., M\}$ in at least one of a plurality of pairs of profiles $\{A_m, C_m\}$, A_m being an experiment profile, C_m being a reference profile, where $m = 1, 2, \ldots, M$, M is the number of pairs of profiles, said method comprising:

adjusting, on a computer, said experiment profile A_m using a differential reference profile calculated between C_m and an average reference profile $\bar{C}$ determined for profile pair $\{A_m, C_m\}$ where $m \in \{1, 2, \ldots, M\}$ to generate a first error-corrected experiment profile A'_m; wherein said average reference profile $\bar{C}$ is an average of reference profiles $\{C_m\}$, $m = 1, 2, \ldots, M$; wherein for each $m \in \{1, 2, ..., M\}$, said first error-corrected experiment profile A'_m comprises data set $\{A'_m(k)\}$, said experiment profile A_m comprises data set $\{A_m(k)\}$, said reference profile C_m comprises data set $\{C_m(k)\}$, and said average reference profile $\bar{C}$ comprises data set $\{\bar{C}(k)\}$, wherein said data set $\{A_m(k)\}$ comprises measurements or transformed measurements of a plurality of different cellular constituents measured in a sample having been subject to a first condition, said data set $\{C_m(k)\}$ comprises measurements or transformed measurements of said plurality of different cellular constituents measured in a sample having been subject to a second condition, wherein $k = 1, 2, \ldots, N$; k is an index of measurements or transformed measurements of cellular constituents, N being the total number of measurements; and

outputting to a user, a user interface device, a computer readable storage medium, or a local or remote computer system; or displaying: said first error-corrected experiment profile A'_m, said data set $\{A'_m(k)\}$, a second error-corrected experiment profile A''_m, or a data set $\{A''_m(k)\}$, wherein said second error-corrected experiment profile A''_m comprises said data set $\{A''_m(k)\}$ obtained by combining said first error-corrected experiment profile A'_m with said experiment profile A_m using a weighing factor $\{w(k)\}$, k = 1, 2, ... , N, wherein $w(k)$ is a weighing factor for the k'th measurement.

187. **(New)** The computer system of claim 147, wherein the method further comprises obtaining said transformed measurements of said data set $\{A_m(k)\}$ and said data set $\{C_m(k)\}$ for an experiment according to the equations:

$$A_m(k) = f(x) = \frac{1n\left[\frac{b^2+2\cdot a^2\cdot XA_m(k)}{a}+2\cdot\sqrt{c^2+b^2\cdot XA_m(k)+a^2\cdot[XA_m(k)]^2}\right]}{a} + d,$$

for $XA_m(k)>0$

and

$$C_m(k) = f(x) = \frac{1n\left[\frac{b^2+2\cdot a^2\cdot XC_m(k)}{a}+2\cdot\sqrt{c^2+b^2\cdot XC_m(k)+a^2\cdot[XC_m(k)]^2}\right]}{a} + d,$$

for $XC_m(k)>0$

where $\{XA_m(k)\}$ and $\{XC_m(k)\}$ are data sets comprising measurements of said plurality of different cellular constituents that when transformed produce said transformed measurements of said plurality of different cellular constituents of said

data set $A_m(k)$ and said data set $C_m(k)$, respectively, where *d* is described by the equation:

$$d = \frac{-1n\left[\frac{b^2}{a}+2\cdot c\right]}{a}$$

and where *a* is the fractional error coefficient of said experiment, *b* is the Poisson error coefficient of said experiment, and *c* is the standard deviation of background noise of said experiment.

188. **(New)** The computer system of claim 158, wherein said processing comprises:

normalizing, transforming, and/or removing nonlinearity from measurements of said plurality of cellular constituents of said data set $\{XA_m(k)\}$ of said experiment profile XA_m, and from measurements of said plurality of cellular constituents of said data set $\{XC_m(k)\}$ of said reference profile XC_m.